Sequence Protocol

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: metaGen Gesellschaft für Genomforschung mbH
 - (B) STREET: Ihnestrasse 63
 - (C) CITY: Berlin
 - (E) COUNTRY: Germany
 - (F) POSTAL CODE (ZIP): D-14195
 - (G) TELEPHONE: (030)-8413 1673
 - (H) FAX: (030)-8413 1674
 - (ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Pancreas Tumor Tissue
 - (iii) Number of sequences: 633
 - (iv) COMPUTER-READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)
- (2) INFORMATION ON SEQ ID NO. 1:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

cttcatcgat agetaceget gettecaace aaageaggag ggggeettea eetgetggte 60 agcagtcact ggcgcccgcc atctcaacta tggctcccgg cttgactata ccctggggga 120 caggaccetg gtcatagaca cettteagge etetteetg etgeetgagg tgatgggete 180 tgaccactgc cctgtgggtg cagtcttgag tgtgtcctct gtgcctgcaa aacagtgccc 240 acctetgtge accegettee teeetgagtt tgcaggcace cagetcaaga teettegett 300 cctagttcct ctcgaacaaa gtcctgtgtt ggagcagtcg acgctgcagc acaacaatca 360 aaccegggta cagacatgee aaaacaaage ccaagtgege tcaaccagge etcageecag 420 tcaggttggc tctagcagag gccagaaaaa cctgaagagc tactttcagc cctcccctag 480 ctgtccccaa gcctctcctg acatagaget gcctagecta ccactgatga gcgccctcat 540 gaccccgaag actccagaag agaaggcagt ggccaaagtg gtgaaggggc aggccaagac 600 ttcagaagcc aaagatgaga aggagttacg gacctcattc tggaagtctg tgctggcggg 660 gecettgege acaecectet gtgggggeca cagggageca tgtgtgatge gtactgtgaa 720 gaagecagga cecaacttgg geegeégett etacatgtgt geeaggeece ggggteetee 780 cactgacccc tecteceggt geaattette etetggagea ggeecagetg aaccaatgga 840 ggcctgggga catctggcat ggtcacccct gcacatgatc tgaggccagc tccccttccc 900 tgagetgeet cetgettete ceteaaagte teetaceett etetteetet tttaageeet 960 ctetteeteg ettteettee tacetagete ettgttggtg agettettgt geettaatce1020 tgtgacccag ccccttacac cactttccac cttcctgtcc gaagtacacg gacactagct1080 gccccaggaa gttgtgtgat tttaaatcac ttctgtcttt gctggaaagt gtatttgtgc1140 ataaataaag totgtgtatt tgtttcaaaa aaaaaaaaaa aaaaaaagga ggtttgaagg1200 gg

(2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1072 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

cctccatcag ctcgccgcgc agcggctgta tttgcggcct gtgcgagtag gcgcttgggc actcagtete ectggegage gaegggeaga aatetegaae eagtggageg cactegtaae 120 ctggatccca gaaggtcgcg aaggcagtac cgtttcctca gcggcggact gctgcagtaa 180 gaatgtcttt tccacctcat ttgaatcgcc ctcccatggg aatcccagca ctcccaccag 240 ggatcccacc cccgcagttt ccaggatttc ctccacctgt acctccaggg accccaatga 300 ttcctgtacc aatgagcatt atggctcctg ctccaactgt cttagtaccc actgtgtcta 360 tqqttqqaaa qcatttgggc gcaagaaagg atcatccagg cttaaaggct aaagaaaatg 420 atgaaaattg tggtcctact accactgttt ttgttggcaa catttccgag aaagcttcag 480 acatqcttat aagacaactc ttagctaaat gtggtttggt tttgagctgg aagagagtac 540 aaggtgcttc cggaaagctt caagccttcg gattctgtga gtacaaggag ccagaatcta 600 ccctccqtqc actcagatta ttacatgacc tqcaaattqg agagaaaaaq ctactcqtta 660 aagttgatgc aaagacaaag gcacagctgg atgaatggaa agcaaagaag aaagcttcta 720 atgggaatgc aaggccagaa actgtcacta atgacgatga agaagccttg gatgaagaaa 780 caaagaggag agatcagatg attaaagggg ctattgaagt tttaattcgt gaatactcca 840 gtgagctaaa tgccccctca caggaatctg attctcaccc ccaggaagaa gaagaaggaa 900 aagaaggagg acattttccg cagatttcca gtggccccac tgatccctta tccactcatc 960 actaaggagg atataaatgc tatagaaatg gaagaagaca aaagagacct gatatctcga1020 gagatcagca aattcagaga cacacataag aaactggaag aagagaaagg ca

- (2) INFORMATION ON SEQ ID NO. 3:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1468 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

gcacgaggta ttatgctgtc gtatggctcc actgcagaaa gcaaaagtaa taagactaat aaaaatatca cctgagaaac ctataacatt ggctgttggt gatggtgcta atgacgtaag 120 catgatacag gaggeecatg ttggeatagg aateatgggt aaagaaggaa gacaggetge 180 aagaaacagt gactatgcaa tagccagatt taagttcctc tccaaattgc tttttgttca 240 tggtcatttt tattatatta gaatagctac ccttgtacag tattttttt ataagaatgt 300 gtgctttatc acaccccagt ttttatatca gttctactgt ttgttttctc agcaaacatt 360 gtatgacage gtgtacetga etttatacaa tatttgtttt aetteectae etattetgat 420 atatagtett ttggaacage atgtagacce teatgtgtta caaaataage ceaccettta 480 tegagacatt agtaaaaace geetettaag tattaaaaca tttetttatt ggaceateet 540 gggcttcagt catgccttta ttttcttttt tggatcctat ttactaatag ggaaagatac 600 atctctgctt ggaaatggcc agatgtttgg aaactggaca tttggcactt tggtcttcac 660 agtcatggtt attacagtca caataaagat ggctctggaa actcattttt ggacttggat 720 agggattete tggccatttt tgggctecca gaatatgtat tttgtgttta tteageteet 840 gtcaagtggt tctgcttggt ttgccataat cctcatggtt gttacatgtc tatttcttga 900 tatcataaag aaggtetttg accgacacet ceacectaca agtactgaaa aggeacagat 960 gtactccaac acagttgctt taagtgacga gttcatcgca ctgcagccat tgtcgagggc1020 aaggaatcag ctgagcaaac ttagcttact gaaacaaatg caggtatcaa gtgcttggac1080 tccatgtgct gtttcccgga aggagaagca gcgtgtgcat ctgttggaag aatgctggaal140 cgagttatag gaagatgtag tccaacccac atcagcaggt gtgaaatctc tctaagtagc1200 ctttgctgca gatgagtatc ctatctggaa caggatgaac ctgccgctct agatacctaa1260 taaatcagca gctggtttta ccaactgaag caggaagtct gctatttatt agcactcttt1320 ggtggtagat ttcactttgt ggctttgggg taagggcttt ttcactcaca aaggaagaga1380 aagcaccttt gaagagactt catctaatga acaaaaaatt ttgtttcata atctttctaa1440 aatgggctca gtaggagtgg gtgtatgg

(2) INFORMATION ON SEQ ID NO. 4:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2331 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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cggctcgaga aaggacctct cccttttcag atgcctggca tgaggcttcc agaaacccag
gttcttccag gagaaataga tgagactcct ctttccaagc caggacatga ccttgccagc 120
atggaggata aaacagagaa atggtcttcc cagcctgaag gtccacttaa attgaaagct 180
tcaagtactg atatgccatc ccagatttct gtggttaatg tggatcaact gtgggaagat 240
tetgteetaa etgteaaatt eeceaaatta atggtaceaa ggtteteett eeetgeeece 300
ageteagagg atgatgtgtt catececact gtgagggaag tgeagtgtee agaggeeaat 360
attgatacag ccctttgtaa ggaaagtccg gggctctggg gagccagcat cctgaaggca 420
ggtgctgggg tccctgggga gcagcctgtg gaccttaacc tgcctttgga agctcccca 480
atttcaaagg tcagagtgca tattcagggt gctcaggttg aaagtcaaga ggtcactata 540
cacagcatag tgacaccaga gtttgtagat ctctcagtac ccaggacttt ttccactcag 600
attgtgcggg aatcagagat ccccacgtca gagattcaaa caccttcgta cggattttcc 660
ttattaaaag tgaaaatccc agagccccac acgcaggdta gagtgtacad aacaatgact 720
caacactcta ggactcagga gggcacagaa gaggctccca tacaagccac cccaggagta 780
gactccattt ctggagatct ccagcctgac actggagaac catttgagat gatctcttcc 840
agegteaatg tactgggaca geaaacacte acatttgaag tteettetgg ceaceagett 900
gcagacaget gttcagatga ggagecagea gaaattettg agttteeece tgatgatage 960
caagaggcaa ccacaccact ggcagatgaa ggcagggctc caaaagacaa accagaaagt1020
aaaaaatctg gtctgctctg gttttggctt ccaaacattg ggttttcctc ttctgttgat1080
gagacaggtg ttgattccaa aaatgacgtc cagagatctg ctcccattca aacacagcct1140
gaggcacgac cagaggcaga actgcctaaa aaacaggaga aggcaggctg gttccgattt1200
cccaaattag ggttctcctc atctcctacc aagaaaagca aaagcaccga agatggggcal260
gagctggaag aacaaaact tcaagaagaa acaatcacgt tttttgatgc ccgagaaagt1320
tteteecetg aagagaagga agagggtgaa etgateggge etgtgggeae tgggetggae1380
tccagagtga tggtgacatc cgcggcaaga acagagttaa tcctgcccga gcaggacaga1440
aaagctgacg atgaaagcaa agggtcaggc ctgggaccaa atgaaggctg agaggtatgg1500
ctcatcagta caagagagat gcaaaaaact aagttggaaa gtaaaggcta cacacacata1560
tggagcaccc catcccacag cacattacat ccacctcact tcacagaacg gagaacagag1620
cagaaatgac cagaacacct ttgtcaccat cacacagccc tcctaaaatg gaaccaaagc1680
ttcccagete ceteaaaget ttggatgeaa agaaggeace etgaetteea caagacacea1740
gaattcacac ggtactcaga ggcactgctg gggaagtttg ttggtcttta ttagataaat1800
ttccagagac ctgtccataa tacccaacag aacatgactg tttctttgag gaaagggtta1860
taatgtetgt ggtgtacaag tegtttttgg tataaettet tteetgetge tgetgettee1920
cggcaaacat agttttccta tttcaggcag agtgcggtat attccaggaa acactgtttc1980
ctactcactt agcttacttc tttgttgaat gcctcactaa tggcaagttt caagatgttt2040
tgggtgacaa tgcacacatg ctgggcaaaa gggtgatggc cagtggctgg cagctgggcc2100
agcagaaget aggacatetg tgagttgtea tteteateta tecatgteea etggeetgee2160
agcateegee agtgeettge cagtgtgeae ggteecacae tgtggeecet gagteeceta2220
atgtacacgc tgcagccaga atgcagatgg agctggcttg gctgttccct ggatggcaa2280
taaagaaagt gctgcatccc aaaaaaaaa aaaaagtaaa aaaaaaagg g
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(2) INFORMATION ON SEQ ID NO. 5:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1925 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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aataaaaaaa attgtattta cttagaagca ttcagaatgt caacaaaaca gccgcaattt
tttttttgca attacagagt ggtattcagt taacagaaca acaattatct tcgtataagc 120
tgcatcagag acaactgaag atgaaaaaaa taaaacccaa aaagaaaacc aaaagaaaaa 180
aaaaaaaaaa acaaaaaaca aaactaccat ccccatatat aactaatttg tgctgtgcac 240
caacaagaac ctgctttaaa tttccatgcc aatttacaac ccccatactg taccaggcaa 300
ggttagtggc tattgaaaat accaccagga cagggctatc taaagacaca ttcggtagtg 360
tgttaactat acaaaaaaag acactgtaca gtttaaaaac aaatcttaca cagccttaca 420
tttcaatttt tttctttaaa aggagtgagt tgtgtacagg ggggttaaat gctttataga 480
caagaaaaaa aaaactgcgc tagaaccaac ttattcatca tcatcatctt cttcttcatc 540
tteatettet teatetteet eeteeteete ateetettea teffeeteat etteeteete 600
ttccttcttt ttcttgcttt tttcagcctt gacaactccc ttttttgctg catcaggctt 660
teetttaget egatatgeag caatateett ttegtatttt teetteaett egeageette 720
ttttcataag gctgcttgtc atctgcagca gtgttattcc acatctctcc cagtttcttc 780
gcaacatcac caatggacag gccaggatgt tctcctttga tttttgggcg atactcagag 840
cagaagagga agaaggccga aggaggcctc ttgggtgcat tgggatcctt gaacttcttt 900
tttgtctccc ctttgggagg gatataggtt ttcatttctc tttcataacg ggccttgtcc 960
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gagcacttct tagaaaactc tgagaagttg actgaagcat ctgggtgctt cttcttatgc1080
tectecegae aagtttgeae aaaaaatgea tatgatgaea ttttgeetet eggettetta1140
ggatctcctt tgcccatgtt tagttatttt tctaaaaaat aaaataaata tttgatgtta1200
gcaataaaat tatgacatat aagaccttaa agtacttagt aagggaatga aaaccaaagt1260
actggttatt taacacagta gcgacatcaa cctccgtaaa atcagacaag aatatggccg1320
tcagggcgat ctcaaaaagt ctagacacaa agatataccc atacagtatt ccctatctat1440
ccgcccgagt ctgctctgaa tgagtatcta actggtcact taaacgattt taaaatctag1500
aacaccattt taaaccaacc aaaccaaagg tcagaaaaca tgctgccaat tcgtggcttt1560
gcactagata gggaataaac aagggcctaa gcgagtcgac tcttcctaat tatgggacct1620
taaaaaaaa aatcaccgtg caccgaaagt ttcaaaaaaac accctctttg cataaaactt1680
tgctccaaag agggagcagc agccagctcc ggtgctcgga acccggttgg gaggtgcggt1740.
gccaccgcga ggcagcctcg tttcctatcg gtttggccct gagatgtatt tctgttctga1800
ctaaacacgt ccggtctgaa gtttctccga gtaaacaagg atgagggaca aaagccactc1860
ctgctcgtgg ctcggtggcc ccctcccca actcgggaag tattttttgg agccgtcaaa1920
gttgg
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(2) INFORMATION ON SEQ ID NO. 6:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1368 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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gtcggggagc gcggggccgg ggcccagggg accccgggcc acggagagcg ggaagaggat 60
ggattgcccg gccctccccc ccggatggaa gaaggaggaa gtgatccgaa aatctgggct 120
aagtgctggc aagagcgatg tctactactt cagtccaagt ggtaagaagt tcagaagcaa 180
gcctcagttg gcaaggtacc tgggaaatac tgttgatctc agcagttttg acttcagaac 240
tggaaagatg atgcctagta aattacagaa gaacaaacag agactgcgaa acgatcctct 300
caatcaaaat aagggtaaac cagacttgaa tacaacattg ccaattagac aaacagcatc 360
aattttcaaa caaccggtaa ccaaagtcac aaatcatcct agtaataaag tgaaatcaga 420
cccacaacga atgaatgaac agccacgtca gcttttctgg gagaagaggc tacaaggact 480
tagtgcatca gatgtaacag aacaaattat aaaaaccatg gaactaccca aaggtcttca 540
aggagttggt ccaggtagca atgatgagac ccttttatct gctgttgcca gtgctttgca 600
cacaagetet gegeeaatea cagggeaagt eteegetget gtggaaaaga accetgetgt 660
ttggcttaac acatctcaac ccctctgcaa agcttttatt gtcacagatg aagacatcag 720
gaaacaggaa gagcgagtac agcaagtacg caagaaattg gaagaagcac tgatggcaga 780
catcttgtcg cgagctgctg atacagaaga gatggatatt gaaatggaca gtggagatga 840
agoctaagaa tatgatcagg taactttoga oogactttoo ooaagagaaa attootagaa 900
attgaacaaa aatgtttcca ctggcttttg cctgtaagaa aaaaaatgta cccgagcaca 960
tagagetttt taatageact aaccaatgee tttttagatg tatttttgat gtatatatet1020
attattcaaa aaatcatgtt tattttgagt cctaggactt aaaattagtc ttttgtaata1080
tcaagcagga ccctaagatg aagctgagct tttgatgcca ggtgcaatct actggaaatg1140
tagcacttac gtaaaacatt tgtttccccc acagttttaa taagaacaga tcaggaattc1200
taaataaatt tcccagttaa agattattgt gacttcactg tatataaaca tatttttata1260
ctttattgaa aggggacacc tgtacattct tccatcatca ctgtaaagac aaataaatga1320
ttatattcac aaaaaaaaa aaaacaccgg ggggggccc gggcccca
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- (2) INFORMATION ON SEQ ID NO. 7:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

gaatgeeett tgggggeeag gggeeeetgg gageeeegee accettteee acttggeegg 60 ggtgeeegea geegeeacee etgeaegeat ggeaggetgg caceeecea gageeeteee120 cacageeage ageetteea cagteaetge eetteeegea gteeeeagee tteeetaegg180 ceteaecege acceeeteag ageeeaggge tgeaaeceet cattateeae cacgeaeaga240 tggtacaget ggggetgaae aaccacatgt ggaaceagag agggteeeag gegeeegagg300 acaagaegea ggaggeagaa tgacegettg teettgeetg accagetggg gaacaaceet360 ggaeegagge ateggeeagg acceatagag caceeggttt tteeetgtge cettttggaa420 attg

- (2) INFORMATION ON SEQ ID NO. 8:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1020 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO.
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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caagtaaatg cagcactagt gggtgggatt gaggctatgc cctggtgcat aaatagagac 60
teagetgtge tggcacacte ageggetetg gacegcatee tageegeega etcacacaag 120
qcaggtgggt gaggaaatcc agagttgcca tggagaaaat tccagtgtca gcattcttgc 180
tccttgtggc cctctcctac actctggcca gagataccac agtcaaacct ggagccaaaa 240
aggacacaaa ggactetega eccaaaetge eccagaceet etecagaggt tggggtgace 300
aactcatctg gactcagaca tatgaagaag ctctatataa atccaagaca agcaacaaac 360
ccttgatgat tattcatcac ttggatgagt gcccacacag tcaagcttta aagaaagtgt 420
ttgctgaaaa taaagaaatc cagaaattgg cagagcagtt tgtcctcctc aatctggttt 480
atgaaacaac tgacaaacac ctttctcctg atggccagta tgtccccagg attatgtttg 540
ttgacccatc tctgacagtt agagccgata tcactggaag atattcaaac cgtctctatg 600
cttacgaacc tgcagataca gctctgttgc ttgacaacat gaagaaagct ctcaagttgc 660
tqaaqactga attgtaaaga aaaaaaatct ccaagccctt ctgtctgtca ggccttgaga 720
cttgaaacca gaagaagtgt gagaagactg gctagtgtgg aagcatagtg aacacactga 780
ttaggttatg gtttaatgtt acaacaacta ttttttaaga aaaacaagtt ttagaaattt 840
qqtttcaagt gtacatgtgt gaaaacaata ttgtatacta ccatagtgag ccatgatttt 900
ctaaaaaaaa aaataaatgt tttgggggtg ttctgttttc tccaaaaaaa aaaaaaaaa 960
aaaaaaaaa aaaaaaaaaa aaaaattgcc cccaagggga cgggttacaa ttgggggggg1020
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- (2) INFORMATION ON SEQ ID NO. 9:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 718 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

tgaaaaagta aactacatt cctagcgtgc ccgtgtcttg cttccggctg acgtgtcttt 60 caggaagagg agctggtgag aagacagcga aatggcgcct ccggcccccg gcccggcctc120 cggcggctcc ggggaggtag acgagctgtt cgacgtaaag aacgccttct acatcggcag180 ctaccagcag tgcataaacg aggcgcacgg gtgaagctgt caagcccaga gagagacgtg240 gagagggacg tcttcctgta tagagcgtac ctggcgcaga ggaagttcgg tgtggtcctg300 gatgagatca agccctcct ggcccctgag ctccaggccg tggcacatt tgctgactac360 ctcgccacg agagtcggag ggacagcatc gtggccgagc tggaccgag gatgacgag420 agcgtggacg tgaccaacac caccttcctg ctcatggccg cctccatcta tctccacgac480 cagaacccgg atgccgcct gagtcggac cgcctggac tcgcccggaa ggagctgaag600 agaatgcagg acctggacg ggatgccacc ctcacccagc tcaaggtct ggtaagcttg660 caacgggtgt aaaagctcaa ggatcctct gattcaggg attggtaaa ttgttcca 718

(2) INFORMATION ON SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

geaggacegt cattgacgcc atgagegege tgetgegget getgegeacg ggtgeeceag 60 ccgctgcgtg cctgcggttg gggaccagtg cagggaccgg gtcgcgccgt gctatggccc 120 tgtaccacac tgaggagcgc ggccagccct gctcgcagaa ttaccgcctc ttctttaaga 180 atgtaactgg tcactacatt tccccctttc atgatattcc tctgaaggtg aactctaaag 240 aggaaaatgg cattcctatg aagaaagcac gaaatgatga atatgagaat ctgtttaata 300 tgattgtaga aatacctcgg tggacaaatg ctaaaatgga gattgccacc aaggagccaa 360 tgaatcccat taaacaatat gtaaaggatg gaaagctacg ctatgtggcg aatatcttcc 420 cttacaaggg ttatatatgg aattatggta ccctccctca gacttgggaa gatccccatg 480 aaaaagataa gagcacgaac tgctttggag ataatgatcc tattgatgtt tgcgaaatag 540 gctcaaagat tctttcttgt ggagaagtta ttcatgtgaa gatccttgga attttggctc 600 ttattgatga aggtgaaaca gattggaaat taattgctat caatgcgaat gatcctgaag 660 cctcaaagtt tcatgatatt gatgatgtta agaagttcaa accgggttac ctggaagcta 720 ctcttaattg gtttagatta tataaggtac cagatggaaa accagaaaac cagtttgctt 780 ttaatggaga attcaaaaac aaggcttttg ctcttgaagt tattaaatcc actcatcaat 840 gttggaaagc attgcttatg aagaagtgta atggaggagc tataaattgc acaaacgtgc 900 agatatetga tagecettte egttgeacte aagaggaage aagateatta gttgaategg 960 tatcatcttc accaaataaa gaaagtaatg aagaagagca agtgtggcac ttccttggca1020 agtgattgaa acatctgaaa ttctgctgtc aagattccca tctctaagga ctccaagtgc1080 tagagacaag ggggtctatg agcatttact gacttcctgt taaaacttca ttttttcaaa1140 1202 aa

(2) INFORMATION ON SEQ ID NO. 11:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1610 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ggagccggga ctcgcgggcg gcggcgggg gcgtcgctgc gcggctggcc ggtgaggccg cggcatgggg cgagtgcagc tcttcgagat cagcctgagc cacggccgcg tcgtctacag 120 ecceggggag cegttggetg ggacegtgeg egtgegeetg ggggeacege tgeegtteeg 180 agccatccgg gtgacctgca taggttcctg cggggtctcc aacaaggcta atgacacage 240 gtgggtagtg gaggagggtt acttcaacag ttccctgtcg ctggcagaca aggggagcct 300 gcccgctgga gagcacagct tccccttcca gttcctgctt cctgccactg cacccacgtc 360 ctttqaqqqt cctttcqgga agatcgtqca ccaggtqaqg gccgccatcc acacgccacg 420 gttttccaag gatcacaagt gcagcctcgt gttctatatc ttgagcccct tgaacctgaa 480 cagcatecea gacattgage aacceaacgt ggeetetgee accaagaagt teteetacaa 540 qctqqtqaaq acgggcagcg tggtcctcac agccagcact gatctccgcg gctatgtggt 600 qqqqcaqqca ctqcaqctqc atqccqacqt tqaqaaccaq tcaqqcaaqq acaccaqccc 660 tgtggtggcc agtctgctgc agaaagtgtc ctataaggcc aagcgctgga tccacgacgt 720 acggaccatt gcggaggtgg agggtgcggg cgtcaaggcc tggcggcggg cgcagtggca 780 cgagcagatc ctggtgcctg ccttgcccca gtcggccctg ccgggctgca gcctcatcca 840 catcgactac tacttacagg tctctctgaa ggcgccggaa gctactgtga ccctcccggt 900 cttcattggc aatattgctg tgaaccatgc cccagtgagc ccccggccag gcctggggct 960 gcctcctggg gccccaccc tggtggtgcc ttccgcacca ccccaggagg aggctgaggc1020 tgaggetgeg getggeggee eccaettett ggacecegte tteeteteea ecaagageca1080 ttcgcagcgg cagcccctgc tggccacctt gagttctgtg cctggtgcgc cggagccctg1140 ccctcaggat ggcagccctg cctcacaccc gctgcaccct cccttgtgca tttcaacagg1200 tgccactgtc ccctactttg cagagggctc cggggggcca gtgcccacta ccagcacctt1260 gattetteet ecagagtaca gttettgggg etacecetat gaggeeceae egtettatga1320 qcagagctgc ggcggcgtgg aacccagcct gacccctgag agctgacccc gtgctgcctt1380 ctccaggcag gcctggcctc tgccctggga ctggggcgcc cagggcctcg tgccttctct1440 cttggcctag cctggcccac tcaggacctg cccagcctct gccagctcct ctgcatccgc1500 cctcttctcc ctggggctgg ggtgggggtg gcagggagct gggacctgga gagacaactc1560

(2) INFORMATION ON SEQ ID NO. 12:

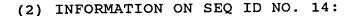
- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2155 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

		+++-~- ~	acacacatac	atacaacaaa	gaatggagga	60
cacgcaagga	tgaggcgggg	tttcgccgtg	gcgcgcatgc	cctaccaaa	gaaggagga	
gtcggaaccc	gaacggaagc	gggctcgcac	cgacgaggtg	ctaccattac	dacaacacca	180
cgaggcggaa	gatgaggacg	acgaggacta	cgtgccctat	gegeegeeae	aggagagaga	240
gcagctactg	ctccagaagc	tgctgcagcg	aagacgcaag	ggagetgegg	aggaagagca	300
gcaggacagc	ggtagtgaac	cccggggaga	tgaggacgac	accongciag	gcccccagcc	360
caacgtcagc	ctcctggatc	agcaccagca	ccttaaagag	aaggetgaag	ttacasasas	420
gtctgccaag	gagaagcagc	tgaaggaaga	agagaagatc	ctggagagtg	regeegaggg	480
ccgagcattg	atgtcagtga	aggagatggc	taagggcatt	acgtatgatg	accccatcaa	
aaccadetdd	actccacccc	gttatgttct	gagcatgtct	gaagagcgac	algagegege	540
acadaadaaa	taccacatco	taataaaaaa	agacggtatc	ccaccaccca	Caagageee	600
caaggaaatg	aagtttcctg	cagccatcct	gagaggcctg	aagaagaaag	gcattcacca	700
CCCSSCSCCC	atteagatee	agggcatccc	caccattcta	tetggeegig	acatgatagg	720
antegettte.	acqqqttcaq	gcaagacact	ggtgttcacg	ttgcccgica	ccatgitting	, 00
cc+cc22C22	gagaagaggt	tacccttctc	aaagcgcgag	gggccctatg	gacttattat	040
at accept ca	cagaaactaa	cccaacaac	ccatggcatc	ctggagtact	actigotigotic	200
t	dacadeteae	cactcctqcq	ctacaccctc	tgcattgggg	geargreegr	300
gaaagagagag	atggagacca	tccgacacgg	tgtacacatg	atggtggcca	ccccggggcg.	1020
catastaast	ttactacaga	agaagatggt	cagcctagac	accigioge	acceggeeee.	1000
ggacgaggct	gaccgcatga	tcgacatggg	cttcgagggt	gacatccgta	CCatcttctc	1140
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gaactttgct	aadadtdccc	ttgtaaagcc	tgtgaccatc	aatgtggggc	gegeeggge	1200
+accaaccta	gatgtcatcc	aggaggtaga	atatgtgaag	gaggaggcca	agatygtgta	132,0
cctactcaaa	tacctacaga	agacaccccc	gcctgtactc	accitiguag	agaagaagge	1300
agacatagac	gccatccacg	agtacctqct	gctcaagggg	gttgaggccg	Lagiciatica	1440
tagacgaggaa	gaccaggagg	aacggactaa	ggccatcgag	gcattccggg	agggcaagaa	1200
gggggcata	gtagccacag	acgttgcctc	caagggcctg	gacttccctg	ccatccagca	1260
	tatgacatgo		tgagaactat	gtacaccgga	ttggccgcac	1620
	ggaaacacag		taccttcatc	aacaaagcgt	gtgatgagtc	1680
	gacctcaaag		agaagccaag	cagaaggtgc	cgcccgtgct	1740
	cattgcgggg	4	gctggacatt	ggaggagagc	gcggctgtgc	1800
	ggcctgggtc		tgactgcccc	aaactcgagg	ctatgcagac	1860
cccccgcggg	accaacatco	gtcgcaagga	ctacctggcc	cacageteca	tggacttctg	1920
caagcaggcc	cttcccttct	ctccaagagg	cctcagtccc	caagactgcc	accagtctac	:1980
ageegacage	cttcccttct	cagaatcago	atttcagctc	agctggcctg	gaatgggcca	2040
acatacagea	gccccccgga	tecetatact	cttcagaatt	actottttto	tttcctttta	2100
ggerggreet	, ggctgcctgt	· caaacctcta	gcccaaaaa	aaaaaaaaa	aaaaa	2155
ccccagctgc	: cattaaagcc	. caaaccccc	. goodaaaaa			

- (2) INFORMATION ON SEQ ID NO. 13:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1743 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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cctqqqcqqq ccctqcqtca ggttqcaqtt tcacttttaq ctctqqqcac ctccaqctcc
tgctcgccgg acggctccca gggagagcag acgcgccaqa cgcgccaccc tcggggcgcc 120
gacggtcacg gagcatgggg tcggcctttg agcgggtagt ccggagagtg gtccaggagc 180
 tggaccatgg tggggagttc atccctgtga ccagcctgca gagctccact ggcttccagc 240
 cctactgcct ggtggttagg aagccctcaa gctcatggtt ctggaaaccc cgttataagt 300
 gtgtcaacct gtctatcaag gacatcctgg agccggatgc cgcggaacca gacgtgcagc 360
qtqgcaggag cttccacttc tacgatgcca tggatgggca gatacagggc agcgtggagc 420
 tggcagcccc aggacaggca aagategcag geggggeege ggtgtetgae agetecagea 480.
 cctcaatgaa tgtgtactcg ctgagtgtgg accctaacac ctggcagact ctgctccatg 540-...
 agaggcacct gcggcagcca gaacacaaag tcctgcagca gctgcgcagc gcggggacaa 600
 cgtgtacgtg gtgactgagg tgctgcagac acagaaggag gtggaagtca cgcgcaccca 660
 caagegggag ggetegggee ggtttteeet geeeggagee aegtgettge agggtgaggg 720
 ccagggccat ctgagccaga agaagacggt caccatcccc tcaggcagca ccctcgcatt 780
 ccgggtggcc cagctggtta ttgactctga cttggacgtc cttctcttcc cggataagaa 840
 gcagaggacc ttccagccac ccgcgacagg ccacaagcgt tccacgagcg aaggcgcctg 900
 gccacagetg cectetggce tetecatgat gaggtgcete cacaacttee tgacagatgg 960
 ggtccctgcg gaggggggt tcactgaaga cttccagggc ctacgggcag aggtggagac1020
 catctccaag gaactggage ttttggacag agagetgtge cagetgetge tggagggeet1080
 ggagggggtg ctgcgggacc agctggccct gcgagccttg gaggaggcgc tggagcaggg1140
 ccagageett gggeeggtgg ageeeetgga eggteeagea ggtgetgtee tggagtgeet1200
 ggtgttgtcc tccggaatgc tggtgccgga actcgctatc cctgttgtct acctgctggg1260
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 tgctgggagc cgcaggccca gggccgcatg tgtgcactct acgcctccct ggcactgcta1560
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 gga
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- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 970 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

eggetegagt gggtttttag tttgtteett etttttgaag teeetteatt teaateettg 60 actetetete coetteeett geccagetet gttgaatget getgtgegeg tgtgagggee120 gctctgcaca cagggccctt gggttgtgtg aactgaaatt ctccctgtat ttgtgagact180 cgcaggagtc cccatctgta gcacaggcaa tgccagtgcc atgctgcagc ctcagaaacc240 aggeetetea etecageage aggeagaace gtgtetgtgg tegggtgetg tecacagete300 tgtctgcctt gttcttgggc ttgagctgga tagaggtggg gtctcttcac cttccctgaa360 ttcagaacag accetgtgcc tggccccagt gtgcccaggc aattccccag gccctcattg420 ggagcccttg gtgttctgag cagcagggcc caggcagcac atgagcagtg cccaggggct480 ccctqcqtqa ggacqgcaag gtgcgatgta tgtctaactt attgatggca ggcagccccc540 tqtqccccct aagcctggcc ctggttattg ctgagctctg tgctcagtgc tgcggcctgg600 ccqtqqctcq tctqttcctt tggggggccc gggcgggttg tgggaatcag tcttcacaga660 cagacgtgag ccaggcggag gactcgttcc ttgcagaggt cagtcctcac ctgcaggtgt720 eggggtgggg gggggcaagg aggggcaggc acacaccatg tetgacetga accegattet780 ggggagcatc ttcccgctcc ggccccacga cctccacagg gttacattgt aatatatatg840 ccccagctaa cctgtctgat ggtggcatct tcctgcagac atttcaaaca tgtaactttt900 aaaaaaaaa

(2) INFORMATION ON SEQ ID NO. 15:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2003 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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gagagatetg aaataacett teecagtggg cagggttgee agggttgagg ggacageaca
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gtgcagctgc ctggcagtgg ctgggacaag gatcttgcag ccagcacaga ggcctcttca 180
aaggeetete eetettggea etecaggeaa ggeaggtgee egetteeeca acacetecag 240
gcagtgaccc tagggcatge eccageaggt eteegageag ceaetgggae eegteteage 300
acatectgge etttgaaagt etgatateet gagaggaggg eaggttttag ggeegeagtt 360
ccagccageg tecccageet ggetteeetg ccatggaete agtagetegt ggggettett 420
accacccacc agccccgctg gggtgcggcc tggctgtggg caaaggagga cttgcctgga 480
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atgctgcctc agacaaaggc agtgagcctt ccctgccaaa gtgcccatcc catgggctcg 660
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tctaatgtgc ccacatgtag cctggcagtc caaagaccaa gaatcaactt gcaaatctgc 840
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                                                                  2003
ataaaaaaaa aaaaaaaaaa aaa
```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2279 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

gattgaatta agcccttggg tttgccccac tgcagcttca agcggaaagg aaggaaccag ttggaccagt ggtcacagac ccaagcaaaa ggcgaccgca atcagcagct gggtctcacc 120 cettteetet gaaccagtga eccaaacett teaccetega ttgggeaace ttggeetggg 180 gcatgtttat caccactgaa gtgacttgca gctatcaaag accagttaga gggtgtgcag 240 caagcacttt ctcaggctgc ccccatccca gaagaggaca cagacactga agaaggtgat 300 gactttgaac tacttgacca gtcagagctg gatcaaattg agagtgaatt gggacttaca 360 caagaccagg aagcagaagc acagcaaaat aagaagtett caggttteet tteaaatetg 420 ctgggaggcc attaatctag gaatcagctt gcaacagagc acaaaaaaca ccaaaaaaat 480 ttcaaacaaa aaaaaaaaaa aaaaaaggaa aagaaaaaaa ttgaactgta agctttaatg 540 attactttag atttgtttta ttttccctcc tgcagtgaat taattggata tatatcagct 600 gacactgata gattgatatt tctgatcgtt atttttgtgt aataagcatg gaaatgaact 660 ttatacacac cactgtgttg tcagagataa atattagggg ttgtttttaa agcaaaaaga 720 aaaaaacaaa aaccaaacta ttaaaatcct cctataaata ttctttttct ttacagtttt 780 tcaagcatgc aaaacagttt attgtaactt actgaaaaat attaacaatt aattgtgaat 840 acatgctgtt accagcttcc ttattcctaa tacctggaaa atttttttt caacggatag 900 attttgatgt aaaaaagacc gaaattatca aggtatctta gttgaaggac ttgggaaata 960 ctatcaaaat taatttctta ggaaaaaatt taaaagtata tttaagtact ctggatagac1020 tgaaacgttt ccatgttatt tctgcagttg tagacttagg cttatttgta aagaagcatg1080 ctccattgac tgccatctct agtcttgcag tgggtggtat taacccatag aaagcaagca1140 gttgtgtatc acatagacaa tggttatgat gtaaacagat tcagttgttt tgttgttcat1200 togtcatatg titgtgatag ggatgttggg agcacagete tattetgeet getcagaett1260 aagttagacc cttatctttt atattatgtc atgaaaaaag tctcctaaaa ttgtgaaact1320 agttcttgat gagtgatgtg atcatcagca ataaagatat aataactctg ttttcttagc1380 ctgtatagag gagaggaact tgcttggctt taaaatatat ttatttgcca tttaagtata1440 aatatgaaat ctgtttctta ttgggaagat agaatatata tattttcctt taaacttttt1500 aaggtcactt ttaaataacc aaatttgatt tatggttttt aacaaaggac taaagagctg1560 aaaccaacct agttttgttt ttgtgatata aactttaagt gtcgagggac catgccagca1620 actaccaaaa atctcttaaa tcttcaggta cagctggcat tttggcagat gcatagagac1680 atctgagacc ctcagaaagg aaggataatc caagaatata ggaaatctgt gttctcttcc1740 tttcatttta tcccttatat ttctaaagac taattataag taatctgaca ttttaatgta1800 gctactctta tttatttttt ctttctgagg tattaaaata tctggactga gttttgccaa1860 atgttaaagg gagaagagtt actgaagact ttgaacactt gctttttgtg attgcttatg1920 tcattagtgc ctcatgactg tgtttgatgt cctttattga tacaaagtga gcctgtgcct1980 tcattatctt gcccatttta atacaaatgg aaacctggtg tttgaaaatc tctgaactgt2040 gtgggttttg gaggaatata cctgaatttt attcaataac agtttctgga caggaagaaa2100 aatacagtta catatttata aaatagtcgt tatcagtatt tttttatgtg tatgtttctt2160 totttaaaac aatattottg gatataaagt agaaaagttt aaaggtoatt tocatttott2220 cactaaggag aaaaaaagtt aaataatcca agtaattaaa gatataagtc actagatga 2279

- (2) INFORMATION ON SEQ ID NO. 17:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 761 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

aaatcttagg gtaagccagc tgccttggaa gcccaccagg gctccagact gcagggaaga 60 agccgggagc aggcagccat acctccactc ttgtcctcaa ggactcagct gtgtggcctt120 ggatttcttt ttgcgggact tgcgccctgc aggacactgg tgttggagtt ggagggtcct180 atcctgcca ggggtgactc ccagggttgc agggggatag ggtggagaag ggtgctgtag240 cccttgcagg cgtgaagtcc tttctgctct cttagcctat tacattagga gtggctgtag240 cttgggttgc aacggtccag gatccccca aaatgggatg gggataattc aggaatcag360 ctgggttggc acagggggg tattccttgg agaggcagga ctcacacaca cccatccaga420 tcagtgtagc ttctccctta ggaagcctct aggacatccc ccatgttaga gtccacatca480 gcaaagctgc tctgcccttg gctactttca cttgggctac ctgccttggg ctacttccac540 tagctgcaac cctgggacgc atgggaggg aggggtgta ccctcaggaa cagtgtggtc600 cttggagggt ctagacagc cctgagcatc accacccag ttattgtgac cccacgtttc660 cacccatcag cctcctgggg tctctgcctg tgtgaacagt agggcccaac ctggaaccag720 atggtacgc catgccggtc ctgcaggag ctcatgcctg g

- (2) INFORMATION ON SEQ ID NO. 18:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1403 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ggtggctttg cctgggtgct gggcctgcgt tctctggctg cttgctgcct gtgtgcgttc 60 cttggtggct ttggcttctg cactccttgg tcgtcaccgc tcaggtcctc cattcacacg 120 aggteetect egetetggee getettgetg etectgtetg aagaaateag actgatttee 180 tcttaagact cctagggatg tggtgaagag ctgggactca agtgcagtcc acggtgtgaa 240 acatgaggga ggtgaggtgt ccgtccactt cccccataaa ggtgtgcatt tcagttaggc 300 tgccccgca cagageagge tteatetget etgccateca gecceatetg gatgtgaggt 360 ggggtggaga catcatgggg tgattgcaga aagggggagt ggcggcccac gcagcttctg 420 ctgaggaget gacegetetg agetgttetg tttegtattg etgetetgtg tetgeatgta 480 ttgtgacgt geggeteeac etetteeage tgetgetaca getgaggeet ggateeegge 540 ctttccctgt gacttacgtg tctgtcaccg gcaggcagcc ctacaaatcc tggtgacctg 600 ctctcccaag aacagagcct gtccccagat gtcccagtag cgatgagtaa cagaggtggc 660 tgtggacttc ctctacttct ccttgctgga tcagggcctt cctgcctccc gctgggcagg 720 totggcottg ctotottggc agggcoccag cocototgac cactotgcag otcaccatge 780 agctgatgcc aaagttgtgg tgtccagtgt gcagcagccc tgggagccac tgccaccttc 840 agaggggttc cttgctgaga cccacattgc ttcacctggc cccaccatgg ctgcttgcct 900 ggcccaacct agcgttctgt gccatgctag agcttgagct gttgctcttc ttcaggggag 960 gaaatagggt ggagagcggg aagggtcttg ctcctaagtg ttgctgctgt ggcttttttg1020 cettetecaa agacgeactg ceaggteeca agetteagae tgetgtgett agtaageaag1080 tqaqaaqcct ggggtttgga gcccacctac tctctggcag catcagcatc ctactcctgg1140 caacatcagg ccaacgtcca ccccagcctc acattgccag atgttggcag aagggctaat1200 attgaccgtc ttgactggct ggagccttca aagccactgg gatgtcctcc aggcacctgg1260 qtcccatgac cagctccccg tctccatagg ggtaggcatt tcactggttt atgaagctcg1320 aqtttcatta aatatgttaa gaatcaaaac tgtctttgtt caggctgcta taacaaaaat1380 ataatagcct gggtggctta aac

(2) INFORMATION ON SEQ ID NO. 19:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1702 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```
gggccgcacc ggagtgtcgg tggtgatggg catcccgagc gtgcggcgcg aggtgcactc > 60
gtacctgact gacactctgc actcgctcat ctccgagctg agcccgcagg agaaggagga 120
ctcggtcatc gtggtgctga tcgccgagac tgactcacag tacacttcgg cagtgacaga 180
gaacatcaag geettgttee ecaeggagat ecattetggg eteetggagg teateteace 240
ctcccccac ttctaccctg acttctcccg cctccgagag tcctttgggg accccaagga 300
gagagtcagg tggaggacca aacagaacct cgattactgc ttcctcatga tgtacgcgca 360
gtccaaaggc atctactacg tgcagctgga ggatgacatc gtggccaagc ccaactacct 420
gagcaccatg aagaactttg cactgcagca gccttcagag gactggatga tcctggagtt 480
ctcccagctg ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 540
gttcattctc atgttctacc gggacaagcc catcgactgg ctcctggacc atattctgtg 600
qqtqaaaqtc tgcaaccccg agaaggatgc gaagactgtg accggcagaa agccaacctg 660
cggatccgct tcaaaccgtc cctcttccag cacgtgggca ctcactcctc gctggctggc 720
aagatccaga aactgaagga caaagacttt ggaaagcagg cgctgcggaa ggagcatgtg 780
aacccgccag cagaggtgag cacgagcctg aagacatacc agcacttcac cctggagaaa 840
gectacetge gegaggaett ettetgggee tteacecetg eegeggggga etteateege 900
ttccgcttct tccaacctct aagactggag cggttcttct tccgcagtgg gaacatcgag 960
cacceggagg acaagetett caacaegtet gtggaggtge tgccettega caacceteag1020
tcagacaagg aggccctgca ggagggccgc accgccaccc tccggtaccc tcggagcccc1080
gacggctacc tccagatcgg ctccttctac aagggagtgg cagagggaga ggtggacccal140
geetteggee etetggaage actgegeete tegateeaga eggaeteese tgtgtgggtg1200
attotgagog agatottoot gaaaaaggoo gactaagotg ogggottotg agggtaccot1260
gtggccagcc ctgaagccca catttctggg ggtgtcgtca ctgccgtccc cggagggcca1320
gatacggccc cgcccaaagg gttctgcctg gcgtcgggct tggggccggcc tggggtccgc1380
cgctggcccg gaggccctag gagctggtgc tgcccccgcc cgccgggccg cggaggaggc1440
aggeggeec caeactgtge etgaggeecg gaaccgtteg caeecegeet geeccagtea1500
ggccgtttta gaagagcttt tacttgggcg cccgccgtct ctggcgcgaa cactggaatg1560
catatactac tttatgtgct gtgtttttta ttcttggata catttgattt tttcacgtaal620
qtccacatat acttctataa gagcgtgact tgtaataaag ggttaatgaa gaaaaaaaaa1680
                                                                  1702
aaaaaaaaa aaaaaaaaaa aa
```

- (2) INFORMATION ON SEQ ID NO. 20:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 802 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

tttttttt ttttttta tttttta ttttaaaaag ggettttatt aaattetee cacaegatgg 60 etectgeaat etgeeacage tetggggegt gteetgtagg gaaaggeet gttteeetg120 aggegggget gggettgtee atgggteege ggaetggeeg tgettggege eetggeggtg180 gtetagetge ttettgeegg geacagaget geggggtetg ggggeacegg gagetaagag240 eaggetetgg tgeaggggt gaggeetgte tettaaecga eaeeetgagg tgeteegag300 atgetggge eaeeetgag ggeaeggga geagetgtg eeggtgetee tteetagee360 agteetggg aaaetaaget egggeeette tttgeaaaga eeggggetge ggtgggtgtg420 ggggaeteat ggggaatgge etgaggaget aegtgtgaag agggeeegg tttgttgget480 geageggeet ggagegeete teteetgage eteagttee ettteegtet aatgaagaae540 atgeegtete ggtgteteag ggetattagg eettgeeete aggaagtgee ettggaegag600 egteatgtta tttteaeaae tgteetgega egttggeetg gggaagtgee ageeagage ggggeeeg720 gtgegeetgg gggtgagggg aggegeeee ggagggeete aeaggaagtt gggeteeeg680 aeeaeeegg gggtgagggg aggegeeee ggagggeete aeaggaagtt gggeteeeg780 aeeaeeagge agggeggget ee

- (2) INFORMATION ON SEQ ID NO. 21:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1647 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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acceptate thickthic contituent thickthit gggtaaggtt gacaceccat
ttattqqaqa agaccccaqc acccqccccc tgaggtctta agggctttgg tgtatccttg 120
gtcacgagcg ctgggccagg aagcagagtt cctgagagcc aagtctagtg gttgagagag 180
gaccetgget gggeetgggg ageaggaage catetgteea getgggeage ecceatgggt 240
ccctggtgca gccccggcca tgtgtccagc gccccatact ccatgagggg ggtctgcacc 300
ccatcacacg ctggttctgc aggtctgcac ccctgtgagg ctgcccctgg ggggcatggg 360
ttctgttggg ctcttgctcc cagcatggat gacccagcga tagcagtcag tgatgcgctt 420
gttgggtgca tgggggccac agcgggtgca gtacacgatg cccagtgcaa gcaggaccac 480
caaaaagaca cacgttggca ccaggagtgc caccagcagc caccggtcat ccctctggct 540
gtgctcggca agaccagcct cccccagggc tgttgggggct gctgtgggag ctggtgaggg 600
cagecacagg gecaacttgg gactggggee atetteeett gggatttggg gggetttgga 660
atggggatgt gtagggctga tgggtgaggt ctggttagtg gggctctgag agggcaggag 720
ggtggggagg gctgcgggct gggtggcagc aggcacagag atttgatggg caggagacac 780
aggggacctg gaggtggtgg tcagagaggg ctgggcagtt gggataatgg gaagctgggt 840
ggcctgggtt ctgaggacaa gggcatctgg ggcttgaggg ggtcgctggg caccgagggt 900
qqtqaccaga ggggcatggt taggtqggat tccaggcaaa tgagtggtgg tctgggtgcc 960
agcgacccgg gtgtctggaa acatggggga ctggtgggca gggaagagct ccggatattt1020
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accgggttgg taggcagaag gcagatctgg atagttggct gcgatcacgg ggatctggtg1140
qtcacqqqac aaaqctqqqt gtqtqqcaqq gatcacaqqa qqctqqtqqq caqaaqqcaq1200
tqtqqqatqc qtqqcaqaqa ccaccacaqq ccqqqtqacq qaqaqcactq aqqaqtqqta1260
ggggaccetg ggggcactga gegggggtgg ceaggtggge teegggtagg gtatetgtgg1320
ctctctgtcc tctgggaagc tcggtctata ggccagggca aagtcaggcg gctgcgtagg1380
ctccatccac aggateccag geateteegt ecagecaceg ttgaageett ccaggeeteg1440
tetteatett ceteateete ecegteatee ageaacteat eteegaggte etgggaacee1500
tgggcaccca tggcccctgc agggctgcag ctgatgccat cagcctccag ctcatgtccc1560
tegetacaat aacactegaa gecaecaaeg tagttgacae acatetgetg geaeacaeeg1620
gcaatctggc actcatctgt gtccaca
                                                                 1647
```

- (2) INFORMATION ON SEQ ID NO. 22:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1170 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO.
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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cctcgctggc agaagagata gaatcagggc tgccccaca gagtgggacc caaggggcta
attggaggca cgaggggacc cctccccagg gccttttcct cctctgcgtc ttccatctac 120
tgaaatggga gaggggtgg ggagcttctg ttctggtgaa gggacccggg caggccccca 180
gcaccccatg ctgacttgga gaaccccaga tctctggggc ccagccaggc agggtgtggg 240
ggcagetgtg ccaatetace teacaggee acceetgee gggcatgeeg tgggateatg 300
qqcaqqqaaq gctctgqggg tcggagacac cgctgcttag cacccccagc cagaacaccc 360
tqaqqqtctc qgggctctgg agagagtggg qcgggaggaa gaattggcac cttcctaggg 420
aaqqaqacqa qcqcttcqcc ttgattctcc gagaaqcctc cgagaaqtgc tttaagtgtg 480
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ccaagtgacg tccactgcct tgtcaccage gacctgcctg tcatgcccac cccctgagga 600
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caccqqccqq gttctqccac agcttcccac gtgcttqctq acatqcqtqt gcctqtqtt 720
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cgaccccacc ccccaaaaaa gctacttctt cattccgtgg tacgattatt ttttttaact1140
aaaggaagat aaaattctat attcttaaaa
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- (2) INFORMATION ON SEQ ID NO. 23:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1259 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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ggagtatcca gataggcgac acgccggcgg gcggctgagg cgggaatggc tgctgtactg
cagegegteg ageggetgte caategagte gtgegtgtgt tgggetgtaa eeegggteee 120
atgaccetee aaggeaccaa cacetaceta gtggggaceg geeccaggag aateeteatt 180
gacactggag aaccagcaat tocagaatac atcagctgtt taaagcaggc totaactgaa 240
tttaacacag caatccagga aattgtagtg actcactggc accgagatca ttctggaggc 300
ataggagata tttgtaaaag catcaataat gacactacct attgcattaa aaaactccca 360
cggaatcctc agagagaaga aattatagga aatggagagc aacaatatgt ttatctgaaa 420
gatggagatg tgattaagac tgagggagcc actctaagag ttctatatac ccctggccac 480
actgatgatc acatggctct actcttagaa gaggaaaatg ctatctttc tggagattgc 540
atcctagggg aaggaacaac ggtatttgaa gacctctatg attatatgaa ctctttaaaa 600
gagttattga aaatcaaagc tgatattata tatccaggac atggcccagt aattcataat 660
gctgaagcta aaattcaaca atacatttct cacagaaata ttcgagagca gcaaattctt 720
acattatttc gtgagaactt tgagaaatca tttacagtaa tggagcttgt aaaaattatt 780
tacaagaata ctcctgagaa tttacatgaa atggctaaac ataatctctt acttcatttg 840
aaaaaactag aaaaagaagg aaaaatattt agcaacacag atcctgacaa gaaatggaaa 900
gctcatcttt agtttcagat taaagaaagc tttgttttat tttgctttga gagaatggta 960
tgttttctta actataggtt attttataga gaatataaaa gtataaaaca ttaaaaataa1020
ccctagatat actttaaaat aatgttatat ttatgctaaa atatgtaaat tacactatac1080
aaccatatga taggttattt ctctaacctt gtcttctaac gttttaccaa aaattcataal140
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tttatctaat ttaaagttga aaaaattttt ggccgttagt tatctattac tagtgatca 1259
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- (2) INFORMATION ON SEQ ID NO. 24:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1021 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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gegtteetee teeggeeete ggteaeegee ageaegegee tgetteeegt etgegegagt
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ttgtgatcag tccatcactg agtggcatgt actccctgcc cttcctcacg gcccctggct 480
cccagetece gggetttgtg ccagtggeee ccatetgeae tgacaaaate aatgetgeea 540
actatgccag tgtgaagact ccagctctga ttgtatatgg agaccaggac cccatgggtc 600
agaccagett tgagcacetg aagcagetge ccaaccaceg ggtgetgate atgaaggggg 660
eggggeacce etgttacetg gacaaaccag aggagtggca tacagggetg etggacttee 720
tgcaggggct ccagtgaagc ccagcactgc tgcagggggt gggctgcctg cctgctctga 780
getetetett geaegetete tettetete caggetetgg eteatgeaca tgeaacaggt 840
gegtetgtet atatgtetgg gttettgtet tttgtggtet gtttgtettt tetacetett 900
tetettgeag tgatagactg agggggtaaa atcaagagga aaaaactete aggaateaag 960
gaacataatc ctgtggaggg taaaccatta catgaggctt ctcccgggtc gttcaagttt1020
                                                                 1021
```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
agcaaaggtt geeggagaee aagateggaa gegtgaaata egaaggeate gagtteattt
aactgaaaac cggctcaagg agcaaggcca tcaggactca gcttttataa aaacaagagg 120
agtgcacttt tgttttgttt tgttcttttt ggaactgtgc ctgggttgga ggtctggaca 180
gggageceag teeegggee catagtggtg egggeaetgg acceeeggge eecaeggagg 240
cegeggtetg aactgettte catgetgeea tetggtggtg attteggtea etteaggeat 300
tgactcaagg cetgectaac tggctgggte gtttetteea teegaceteg tttetttet 360
ttcctatgtt cttttgttca gtgaatatcc ctagagctcc taccatatgt caggccctat 420
gecteacet gagaacgeag tgggeatgag gtggaeetgt ttgetgggaa ceeeaggtea 480
eccetttte ttectaetet gtgeetggag cateatgtee acceetgeag ateettggaa 540
aagaaaatgt ttatgttgca gggtattgca tggtcacgag tgagggcagg cccctgggga 600
cacatotgoo cacagotgoa caggocaggg cgcaggcaca totgttggtt otcaggoote 660
agataaaacc atctccgcat catatggcca gtgaccgctt tctcccttca agaaaattct 720
gtggctgtgc agtactttga agttttaatt attaacctgc tttaattaaa gcagtttcct 780
ttcttataaa gtggaatcac caaatcttat cacacagagc acagtcctgt agttacccag 840
cecgetecag cagtgeggga gattgtaagg aageggtgge ggetggtgaa gcaagtetea 900
catgtcggcg ttcttggcca atggatacaa agataaagaa aatgttgcct ttttctagga 960
actgtcagaa atcctcatgc ctttcaagac ttctgtgaat gacttgaatt ttttattccc1020
tgcctagggt ctgtgaacga ggcctgtctc ttccctgggg tttctttcca tggcctttat1080
ttctcctctt ccagtgggag ttttgcaggc tcttctctgt ggaaacttca cgagcgttgg1140
ctgggcctcg gcttcgctgg agtgtactcc agggtgaagg cagagtggga tttgagaccc1200
aggitaggca cgacccaggc tgagaaggga cgtttccatc attcacagtg ccctcccac1260
agcactacct cagecegage eccaecetea etectaeece acceegegat egteaggggt1320
gccacggtgg gccggagggt gccccgtcgg ggcttgttcc tgttgccggt ccctgaaaaa1380
                                                                  1407
gcttttcccc ttttgaaatt caagcac
```

(2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ctctcggctc cgcctggcag cagctccgcc gcccagaggc gtccgagacc ctccgactcg 60 tgggtacgca taggcctcgc cagcgagcct tgcccaggca acgagtcgcc agcccgcccc120 ctcgccgcgg gctaggtctc acctcgccac cagtacgtct tggacaagta gtgccaggtc180 tgatgccggg tgtggtgagt gccgccggga cccaggtgcg ccgcctcgat gaggtcccgg240 cgtcgctccg gctgcagcac cacctccagc tccgcgaagg tcttgc

- (2) INFORMATION ON SEQ ID NO. 27:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 815 base pairs
 - (B) TYPE: Nucleic acid (C) STRAND: individual

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

cgcctcgttt gcactgggtg ctggacagcc gacgcaacta caaatggggc ggagtttcgg 60 cactggagca gctaatttgc atataggaat gagctccac aaacacgaga agttccagca120 agttcgccac ttccggttct cctggctatc caatagcatc gagtggagca tccccggaag180 tgaagcacgcg gaggacgacc tttttccggt tccggcctgg cgagagtttg tgcggcgaca240 tccccctgcg cctccaggcc accgaggtcc gtatctgccc tgtggagtc aacccaact360 tcgtggcgcg tatgatacct aaagtggagt ggtcggcgt cctggaggcg gccgataact420 tgcgtctgat ccaggtgccg aaagggccgg ttgagggata tgaggagattc480 tgaggaccat gcaccacctg ctgctggagg tggaggtgggg gccgataact420 tgaggaccat gcaccacctg ctgctggagg tggaggtaa tgagggagaat gaggagtttc480 tgaggaaccat gcaccacctg ctgctggagg tggaagtga agagggcacc ctgcagtgcc540 cggaatctgg acgtatgttc cccatcagcc gcgggatccc caacatgctg ctgagtgaag600 aggaaactga gagttgattg tgccaggcgc cagtttttct tgttatgact gtgtattttt660 gttgatcaa acccaaacaa aatgttttt agctcggtat tatatattt tttctcatta aaggtttaaa780 accaaaaaaa aaaaaaaaa aaaaaaaa ccgacg

(2) INFORMATION ON SEQ ID NO. 28:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

tttctcgaac cttctcttt ctttctttt tgcactgtgc aaatatattg actttatttg 60 tctcctttca ggagcctcac agacatatcc aggtaaaaag atcgttaaat aaatgccttc120 agccatcgca atgcaaaaat aaatatcaat cctccagacg cagtagcagc cgcgctgcgc180 ccaaagtccc aacggccacg cctaacaatt ataaaagtgt tcagcgagag tgttggcgt240 agtgtgaatg ggtgtgcgct ggggggcacg gtggagcggt gtgcaaaatc ggagttgcaa300 accatcggac aagggcatgg agtggctacc cgccgccgac tcagcgcggg cgcgcctccc360 cgcacacact cacagcagag ttcgcactgg gaagagttaa aaaataaaca tttacaagga420 cgagcgaaagc ggccccgctc ccggcgccc cgggccagg cgagcgcgc gaggggcgca480 ccgaccggt cgcagcggc cgggagtccg aagcgccca ggagcgccg gtcccgggc cttgcggg

- (2) INFORMATION ON SEQ ID NO. 29:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

gcaagatggc tgccctgaca gcggagattt tgcagcactc cagagcctgc tcaaggcctc 60 ctcgaaagat gttgtcagac agctgtgtca agaaagcttt tccagttcag cccttggctt120 gaaaaaactc ttggatgtta catgttccag cttgtctgtg acccaggagg aggcagagga180 actgctccag gctctgcacc gcctcactag gctggtggca ttccgtgacc tgtcctctct ttccagaaaa tttccaccaa aacctcaaaa acctgctgac300 caagatcatc ctggtcgatc tggactggag aggtgatatc aaaacctcct cagacagcat420 cagccgcatg gccgttgccc cacctggcct ggttccagat ggaaggttcc aggaggttc480 ccaggctatg ggg

- (2) INFORMATION ON SEQ ID NO. 30:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1063 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN

- (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
egecteece tecaactete aacceaette tecagecage gececagece tecegeegee
cgctcgcagg tcccgaggag cgcagactgt gtccctgaca atgggaacag ccgacagtga 120
tgagatggcc ccggaggccc cacagcacac ccacatcgat gtgcacatcc accaggagtc 180
tgccctggcc aagetectgc teacetgetg etetgegetg eggeeceggg ceacecagge 240
caggggcage ageoggetge tggtggcete gtgggtgatg cagategtge tggggatett 300
gagtgcagtc ctaggaggat ttttctacat ccgcgactac accetectcg tcaceteggg 360
agetgecate tggacagggg etgtggetgt getggetgga getgetgeet teatttacga 420
gaaacggggt ggtacatact gggccctgct gaggactctg ctagcgctgg cagctttctc 480
cacagocato gotgocotoa aactitiggaa tgaagatito ogatatiggot actotitatia 540
caacagtgcc tgccgcatct ccagctcgag tgactggaac actccagccc ccactcagag 600
tccagaagaa gtcagaaggc tacacctatg tacctccttc atggacatgc tgaaggcctt 660
gttcagaacc cttcaggcca tgctcttggg tgtctggatt ctgctgcttc tggcatctct 720
ggcccctctg tggctgtact gctggagaat gttcccaacc aaagggaaaa gagaccagaa 780
ggaaatgttg gaagtgagtg gaatctagcc atgcctctcc tgattattag tgcctggtgc 840
ttctgcaccg ggcgtccctg catctgactg ctggaagaag aaccagactg aggaaaagag 900
getetteaac agecceagtt atcetggeec catgacegtg gecacageec tgetecagea 960
geacttgeec attecttaca eccetteece atectgetee getteatgte eccteetgag1020
tagtcatgtg ataataaact ctcatgttat tgttcccaaa aaa
```

- (2) INFORMATION ON SEQ ID NO. 31:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
cggctcgagg cggcgatg gcggcgggc tggcgcggt cctgttgct ctcgggctct 60 cggccggcgg gcccgcgcg gcaggtgcag cgaagatgaa ggtggtggag gagcccaacg120 cgtttggggt gaacaacccg ttcttgcct aggccagtcg cctccaggc aagagggatc180 cttcaccgt gtctggacc gtgcatctct tccgactct gggcaagtgc ttcagcctgg240 tggagtcac gtacaagtat gagttctgc cgttcacaa cgtgacccag cacgagcaga300 ccttccgctg gaacgcctac agtgggatcc tcggcatctg gcacgagtgg gagatcgcca360 acaacactt cacgggcatg tggaggg acggtgacca cggcaactg cgtctaaggg gt 472
```

(2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2568 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
catctetetg cagtgeeete etegeetgtg cagecegege acceaeagge teaeceetee 60
tgcgggctgc cagaagcccc ctccagcagg gcctctctcc gtggccccag cttcactctc 120
teceteagea catgecetge tggaggeece ageceteegt ggacageagg ggeeaegtgg 180
agecegggee geteaceege gacceagtge tggeegeett ettggtgeea aaceeeette 240
ccccacccag agactgggca gctgtgtctg gttcgttctt tgcactaacc acatttgtca 300
tetetaggge aggetgggge tgegggetga gggggaeege tggeaeeeee etteeeteee 360
ttottggtto catttocato catgacaggt acagcatoco aggagecegg cetgagggge 420
tggacccgag ccggctgtga acatccctca gcccctgctg tccccccttg ggactaacca 480
ctaacctcac ccccaaactc cacgggtgcc cctagctggc ccagagccgg cagtgtgagc 540
ccaagtccgg gctggagccg aggccggagc agctgtctgg gagtcaaggc tgcagtagcg 600
tttcttcatg gggtgctcca gggggtgcca cagaccgaca ggcagcccaa gggcctggac 660
accectecce aggeaggtge tgeeccagga ggaetgteet egggaatgaa eeteeegegg 720
getttggact gaggteectg tggeeteggt etecteecea tgaagtggga gegaggetee 780
ccaatggtgc ttttggcttt agtgtacgat gtttgctgtg cttcccgccg tggagggcag 840
agecacecca cateaggate ggaegtgeta ececteeegg teeeggeeet ggeeeageea 900
gcccagccct cgaggctcga tgcctgtgcc aaggccaggg gcagccagag ggcagctgga 960
tggccacgtg caggggtcaa ggctgggccc tgcagtgggg cgggccgcca gccccagcag1020
tttacagacg catggctctt cctcccagag cagccggcag ctacctggac cggaaatgtc1080
ctcatcccct ccctggggcc aggctctgcc ctggccttcc tctgtgaacc cctcctttct1140
ttgtgctggt gtctgggacc aaaaaggggg aatatgggag ggcagagtgg ggaggggagt1200
ccatgggcct ggggccccaa gccggggcgt ctgagctccc caggcatgac caaacctcag1260
tggagggcc tctgcttcag gccccgcctg gctgacattc tgagcccccc tcggaggccc1320
cgccacagcc aacctgccca gtctttcctc tgggcttgac ccgccaggga gttctccagg1380
cctagggcca ggagagaggc cctggcaccc tggcgtgggt gcccgccaaa cgccctgcga1440
ccgctcagaa gcacaaatgc tgtccatggc cgtgaggctg cctgccaggt gaatggacat1500
agcgtgagag gcggtgaggc cagggcttcc agcctcgtgc tgtctcggga ctcctgaccg1560
tggtgtgcgt gtgtgcccgt ctgtgacttt ctactcacca aggttgaaga aaggaaacgg1620
ggaaaatcaa aaggggttca aaccccacct cagtaggtgg aggggagcgc ctgccattgg1680
ttgtattttt gttctgagtt ttcggtgccg tgttcctaac tactccatcc catgacctcg1740
ccacacctac tggggcatct ggctggtgcc tgctgccatg gccagccccc actctcaccc1800
tgcacagggg gtcttgcagc ccccaggccc acagcctcgt tgggaggaca gggtggccct1860
ggggacaaga gggaggagcc caggggctta cctcactgag agtgctcccc agcaggcatc1920
cactacccca gggcccccca catgtcatgg caaggttggt agtgaatggg cctggttggg1980
agcagecect ggeceattge ecacecacee ateteaetat geaattegag ttecaagcaa2040
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catttgctc tgccctgggg ccagctctge cccagccctg agaggggtgg tgaggcagcc2100 ccctggacc cagaaccca gacaagggg caggcgggg accagggct ctcctgtggg2160 atcttgtt tgtgtttaac cataatggtt gtgtactgaa ccacttcata tttgttatat2220 ataatatata tatatataat ctccttaaga ctcagcctcc tggtttaccc ccccggcctg2280 ggcatctgac ctccccacc ccagtgtgat ttaacatcca ggaactgagg cctgaaccat2340 tttgcatttc cccctcctc agcctctgta gggccatggc tgtatgtact gtcgctgtgt2400 tttttgttt ttttagaact gggtttgggg gctgatttt atttcttgg gggcttttt2460 tcttggcaaa tactaaaaat ctcgtcaatg taatttctgt ggtttctatt cagcttgggt2520 ttcatgttt aaaataaat ttaaaaagca aaaaaaaaa aaaaaaaa 2568

- (2) INFORMATION ON SEQ ID NO. 33:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

cgcgatggcg gcggggctgg cgcggctcct gttgctcctc gggctctcgg ccggcgggcc 60 cgcgccggca ggtgcagcga agatgaaggt ggtggaggag cccaacgcgt ttgggtgagc120 agcctcgcgg gctggcggct cgagcgggg acggcccggg cccgttcccc gctgaccttg180 ccgcttcccg taggtggaac aacccgttct tgcctcaggc cagtcgcctc caggccaag 239

- (2) INFORMATION ON SEQ ID NO. 34:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

- (2) INFORMATION ON SEQ ID NO. 35:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 641 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gagagcagta ggtgttagca gcttggtcgc gacaggggcg ctaggtagag cgccgggacc 60 tgtgacaggg ctggtagcag cgcagaggaa aggcggcttt tagccaggta tttcagtgtc120 tgtagacaag atggaatcat ctccatttaa tagacggcaa tggacctcac tatcattgag180 ggtaacagcc aaagaacttt ctcttgtcaa caagaacaag tcatcggcta ttgtggaaat240 attctccaag taccagaaag cagctgaaga aacaaacatg gagaagaaga gaagtaacac300 cgaaaatctc tcccagcact ttagaaaggg gaccctgact gtgttaaaga agaagtggga360 gaacccaggg ctgggagcag agtctcacac agactctcta cggaacagca gcactgagat420 taggcacaga gcagaccatc ctcctgctga agtgacaagc cacgctgctt ctggagccaa480 agctgaccaa gaagaacaaa tccacccag atctagactc aggtcacctc ctgaagccct540 cgttcagggt cgatatcccc acatcaagga cggtgaggat cttaaagacc actcaacaga600 aagtaaaaaa atggaaaatt gtctaggaga atccaggcat g

- (2) INFORMATION ON SEQ ID NO. 36:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

aagttgatga cctacgctct tacttctgct tgccaggagt aactgaaagc aaacaccaca 60 gtctgttgtt tattagcttt taaaggcttg tcaacattcc ttgttaacaa tttctttttg120 ggtagccttt tataaaatgc gtaggtgatg agtgatccag cagacaaggc ggctcgagcc180 gattcggctc gagcggctcg aggtaaaaga aaaaaaaatg tggaggaaaa catggcctac240 tcagctttga tggaagtggc tggttactgc ttaatagaga gaatgctttg gaatcctatg300 ttgaaaataa aaagtgtttg gttgtgcagt tatgcggtca tggtcattcc cagacagttg360 gctaaggttt agtggtcctc t

- (2) INFORMATION ON SEQ ID NO. 37:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1539 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
ctggggacag gaagcccctg taccattatg gtcggggcat gaatcccgct gacaaaccag 60
cctgggcccg agaggtaaaa gagagaacaa ggatgaacaa gcagcagaac tctcccttgg 120
ccaagagcaa gccaggcagc acggggcctg agcccccaag cccccaggcc tccccagggc 180
ccccaggect cccctgggcc cccaaaccct accacaaatt catggeette aagteetttg 240
ccgacctccc ccaccgccct ctgctggtcg acctgacagt agaggagggg cagcggctca 300
aggtcatcta tggctccagt gctggcttcc atgctgtgga tgtcgactcg gggaacagct 360
atgacatcta catccctqtg cacatccaga gccagatcac gccccatgcc atcatcttcc 420
tececaacae egacggeatg gagatgetge tgtgetaega ggacgagggt gtetaegtea 480
acacqtacqq qcqcatcatt aaggatgtgg tgctgcagtg gggggagatg cctacttctg 540
tggcctacat ctgctccaac cagataatgg gctggggtga gaaagccatt gagatccgct 600
ctgtggagac gggccacctc gacggggtct tcatgcacaa acgagctcag aggctcaagt 660
tectgtgtga geggaatgac aaggtgtttt ttgeetcagt eegetetggg ggeaqeagee 720
aagtttactt catgactctg aaccgtaact gcatcatgaa ctggtgacgg ggccctgggc 780
tggggctgtc ccacactgga cccagctctc cccctgcagc caggcttccc gggccgcccc 840
tettteeect eeetgggett ttgettttae tggtttgatt teaetggage etgetgggaa 900
cgtgacctct gacccctgat gctttcgtga tcacgtgacc atcctcttcc ccaacatgtc 960
ctcttcccaa aactgtgcct gtccccagct tctggggagg gacacagctt ccccttccca1020
ggaattgagt gggcctagcc cctccccct tttctccatt tgagaggaga gtgcttgggg1080
cttgaacccc ttaccccact gctgctgact gggcagggcc ctggacccct ttatttgcac1140
gtcaggggag ccggctcccc ccttgaatgt accagaccct ggggggggtc actgggccct1200
agatttttgg ggggtcacca gccactccag gggcagggac catttcttca ttttctgaaa1260
gcactttaat gattcccctg ccccaaact ccagggaatg gagggggag cccgccagcc1320
aaaacatgcc ccccattccg gaccccctc tcctcttcta gcccatgccc ttccccggtg1380
gagggaggga gcagggagcc ctcactctcc acgccccttg cttgcatccg catatagtgt1440
gagcagcaag taaccettet ceteetteee cagteaceee teetcaatgt agtggeettg1500
aattgtcttt attaacaaac aggatatcca aggtcgagc
                                                                 1539
```

(2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2195 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

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geteegagga aggeetgtgg gagtetegga gaegtgtetg tetgtgagge getgggtgea
egtececagg getetggget aggaaggeag eggegaggtg cetececaeg taccectege 120
gggcccagcc gagcaacgtg gggcgaaggc ggcggcgaag gcccgggctg ggagcgttgg 180
eggeeggagt eccageeatg geggagtetg tggagegeet geageagegg gteeaggage 240
tggagcggga acttgcccag gagaggagtc tgcaggtccc gaggagcggc gacggagggg 300
gcggccgggt ccgcatcgag aagatgagct cagaggtggt ggattcgaat ccctacagcc 360
gcttgatggc attgaaacga atgggaattg taagcgacta tgagaaaatc cgtacctttg 420
ccgtagcaat agtaggtgtt ggtggagtag gtagtgtgac tgctgaaatg ctgacaagat 480
gtggcattgg taagttgcta ctctttgatt atgacaaggt ggaactagcc aatatgaata 540
gacttttctt ccaacctcat caagcaggat taagtaaagt tcaagcagca gaacatactc 600
tgaggaacat taatcctgat gttctttttg aagtacacaa ctataatata accacagtgg 660
aaaactttca acatttcatg gatagaataa gtaatggtgg gttagaagaa ggaaaacctg 720
ttgatctagt tcttagctgt gtggacaatt ttgaagctcg aatgacaata aatacagctt 780
gtaatgaact tggacaaaca tggatggaat ctggggtcag tgaaaatgca gtttcagggc 840
atatacaget tataatteet ggagaatetg ettgttttge gtgtgeteea eeaettgtag 900
ttgctgcaaa tattgatgaa aagactctga aacgagaagg tgtttgtgca gccagtcttc 960
ctaccactat gggtgtggtt gctgggatct tagtacaaaa cgtgttaaag tttctgttaa1020
attttggtac tgttagtttt taccttggat acaatgcaat gcaggatttt tttcctacta1080
tgtccatgaa gccaaatcct cagtgtgatg acagaaattg caggaagcag caggaggaat1140
ataagaaaaa ggtagcagca ctgcctaaac aagaggttat acaagaagag gaagagataa1200
tccatgaaga taatgaatgg ggtattgagc tggtatctga ggtttcagaa gaggaactga1260
aaaatttttc aggtccagtt ccagacttac ctgaaggaat tacagtggca tacacaattc1320
caaaaaagca agaagattot gtcactgagt taacagtgga agattotggt gaaagottgg1380
aagacctcat ggccaaaatg aagaatatgt agataatgga ctgggatata ttgtatttct1440
catgttaaag cctcttccct tgaaattaaa aaaaaatttt aactgataaa acttagggca1500
acattaatta atgtatatto ttacctgaat tgttatactt tttgaaaatc ctgtgacttg1560
cctgtttctc cccgctccaa cgaaatcatt aactctccta aaatgtgttt cattctagta1620
agaaaacctc aaaggatatt gtaggatata aatcttactt gaaaacatag ctgttgaaat1680
gttttggcct tttggagtgg gggaaggaca aatctgatcc tgtaatcttt ttctttccag1740
taatcccttg tgtctgttgc atgaggacat ggacaataaa gtagtatatg atcctcagat1800
acagggagaa ggacaaggca tacagcttat tgattagagc tggcaagcat ctgctcatta1860
tgtttggaat tgctttctat aagaaaattg cccactacta ctaacttgat caacaatgaa1920
ttcaaaatag ttaacctatg aaataacatc ctctcaaatg tttgctgatg aagtacaagt1980
tgaaatgtag ttattggaaa agtctgtaac ctgtggatca tatatattca aagtgagaca2040
aaggcaaata aaaagcagct attttcatga atagaaaaaa aaaaaatttc aggaagtata2100
aattatatto tgcaccgaac aaggaacaga aattattgca totgtggaag catatatotg2160
ggagttacta ttactttact ggaagggcca agggc
```

- (2) INFORMATION ON SEQ ID NO. 39:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1409 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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qtttqctqtc cttttttaaa ggattccaaq ccatqtqaaa ttcccttctq qatqtqattc 60
tgggtcgcaa gtccttattt atatgtgagg ctggggaatg ggctgggggt attggcagtc 120
cttttgcagg gcagtgtgtg tggtggggtg acaccgctgt ggcttagccc aaqacactcc 180
cagaggaaaa cactgcagaa ggaactggtt tgcagactgt ggaaggatct gcagttttgt 240
ttttgaccaa aaaaataata ataagttagc tctgaagggc agagggaata cccaaqcccc 300
tgatgcctat gagaagtccc tggacttcaa ccctcctgtt gtttggcctt agcccagagg 360
gagctgctca cctgagcacc cttgggggtg ggcagagagg cagggtggga ttttagagtt 420
agtgtctgtg cgggggcagc cctgagcctg gagttgagac tttggggtct cttagtttgg 480
aggtgttgag tgcatttgtg cccctgcctg gttgagagct tcttggtacc tcttgccacc 540
cetteteact geoetgacee aacceeactg gacettgatg etgegaggag tggtgteetg 600
acggactcag cactcccgcc tgatgtattg gatcatagga gagcacttgc tctcctgcct 660
ctgccaggag agggcttgtt cctccaactc taggaggcca ggcaagcatg gacaggagcc 720
aagggagcag ggtcattaac tttttcttct ttgcaaagtg ggcacttggc atcagggtcc 780
caatcaccag aaagcaccaa agcccctggc accccaccca ctccatccta cccagggacc 840
ccaagtaggc aactgttatg gcagtgggtc cagcccaggc cagcactgcc agcctcctct 900
ccctgcagta ggcaccagct ctacctcccc cggcaggcaa tgtcctggct tctcagccca 960
gcaccatctg ttcccctaga cttctcaggg gccagcccag tctgggccac cctttgtttc1020
cctcatcctc ggctcccaca caggtgacag acccagcaga tagcttctct ctgggaaagg1080
ttggatgctg ccttacatcc ccttctagcc ctcctcccat ccacacaca aggcacccac1140
ccacaccagg tcggcttgtt tctcacatgt agggagagag gggagaccaa cccctttgtg1200
tettttgaaa taegaagaaa aatgtgtgtt caggageatg aeteeagtge tgegetettg1260
ggcctagttc agtctgtctt gtctcaaatc taggcatttt tgcttcaatt ttatttttt1320
taaaacattt ttttgggtgt cccgttggta ttggaataat ttggctaaca ttggtaaaag1380
gtaagggggt taaaatataa ggtaatttt
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(2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1084 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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ggaatcttta agcaatcata cggggaaaaa gggcccatca ccttcaaagg agccacaatt 60
agacteetea acagacatga ttgaggetgg aagataaggg aatggtatet tetteaaage 120
cgaaagaata ggaccacacc tgccaggatt tggttgttta aatataaatc tgatcacccc 180
cctgcttaga acccttctgc tttctattac ccctcattta aaatgtaaac tcttcacctt 240
ggtttatgag aactggttct tgccttcccc ttgaacctca ttaaatggtg atttcttgct 300
aageteeage eegagtggte teeteteage ttetaatttt gtgetettte etgeeetttt 360
cctgggcctt ctcagctctc caccccacc actcttgact caggtggtgt ccttcttcct 420
caagtettga caatteeegg geeetteagt eeetgageag tetaettetg tgtetgteae 480
cacatettgt etttteeest cattgeattt attgeagttt atatatatge taettttaet 540
tgttcatttc tgtctcccct accaggctgt aaatgagggc agaaaccttg tttgttttat 600
tcaccatcat gtaccaagtg cttggcacat agtgggcctt cattaaatgt ttgttgaata 660
aaagagggaa gaaggcaagc caaccttagc tacaatccta ccttttgata aaatgttcct 720
tttgacaata tacacggatt attatttgta ctttgttttt ccatgtgttt tgcttttatc 780
cactggcatt tttagctcct tgaagacata tcatgtgtga gataacttcc ttcacatctc 840
ccatggtccc tagcaaaatg ctaggcctgt agtagtcaag gtgctcaata aatatttgtt 900
tgggtggttt gtgagccttg ctgccaagtc ctgcctttgg gtcgacatag tatggaagta 960
tttgagagag agaacettte cacteceact gecaggattt tgtattgeca tegggtgeca1020
aaaa
                                                              1084
```

(2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2860 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

teetggetga ttetttteet ggeagtteee ettatgaggg ttacaactat ggeteetttg 60 agaatgtttc tggatctacc gatggtctgg ttgacagcgc tggcactggg gacctctctg 120 acggttacca gggccgctcc tttgaaccgg taggtactcg gccccgagtg gactccatga 180 gctctgtgga ggaggatgac tacgacacat tgaccgacat cgattccgac aagaatgtca 240 ttcgcaccaa gcaatacctc tatgtggctg acctggcacg gaaggacaag cgtgttctgc 300 ggaaaaagta ccagatctac ttctggaaca ttgccaccat tgctgtcttc tatgcccttc 360 ctgtggtgca gctggtgatc acctaccaga cggtggtgaa tgtcacaggg aatcaggaca 420 tetgetaeta caactteete tgegeeeace caetgggeaa teteagegee tteaacaaca 480 tectcageaa cetggggtae atectgetgg ggetgetttt cetgeteate atectgeaac 540 gggagatcaa ccacaacegg gccctgctgc gcaatgacct ctgtgccctg gaatgtggga 600 tccccaaaca ctttgggctt ttctacgcca tgggcacagc cctgatgatg gaggggctgc 660 tcagtgcttg cgatcatgtg tgccccaact ataccaattt ccagtttgac acatcgttca 720 tgtacatgat cgccggactc tgcatgctga agctctacca gaagcggcac-ccggacatca 780 acgccagcgc ctacagtgcc tacgcctgcc tggccattgt catcttcttc tctgtgctgg 840 gcgtggtctt tggcaaaggg aacacggcgt tctggatcgt cttctccatc attcacatca 900 togccaccot getectcage acgcagetet attacatggg ceggtggaaa etggactegg 960 ggatcttccg ccgcatcctc cacgtgctct acacagactg catccggcag tgcagcgggc1020 cgctctacgt ggaccgcatg gtgctgctgg tcatgggcaa cgtcatcaac tggtcqctgg1080 ctgcctatgg gcttatcatg cgccccaatg atttcgcttc ctacttgttg gccattggcall40

tctqcaacct gctcctttac ttcgccttct acatcatcat gaagctccgg agtggggaga1200 qqatcaagct catccccctg ctctgcatcg tttgcacctc cgtggtctgg ggcttcgcgc1260 tottottott ottocaggga otcagoacct ggcagaaaac cootgcagag togagggagc1320 acaaccqqqa ctgcatcctc ctcqacttct ttqacqacca cqacatctqq cacttcctct1380 cctccatcqc catqttcggg tccttcctgg tgttgctgac actggatgac gacctggata1440 ctgtgcagcg ggacaagatc tatgtcttct agcaggagct gggcccttcg cttcacctca1500 aggggcctg agctcctttg tgtcatagac cggtcactct gtcgtgctgt ggggatgagt1560 cccagcaccg ctgcccagca ctggatggca gcaggacagc caggtctagc ttaggcttgg1620 cctgggacag ccatggggtg gcatggaacc ttgcagctgc cctctgccga ggagcaggcc1680 tgctcccctg ggacccccag atgttggcca aattgctgct ttcttctcag tgttggggcc1740 ttccatgggc ccctgtcctt tggctctcca tttgtccctt tgcaagagga aggatggaag1800 qqacaccete eccattteat geettgeatt ttgeeegtee teeteecae aatgeeecag1860 cctgggacct aaggestett tttestessa tastessact ccagggesta gtetgggges1920 tgaatctctg tcctgtatca gggccccagt tctctttggg ctgtccctgg ctgccatcac1980 tgcccattcc agtcagccag gatggatggg ggtatgagat tttggggggtt ggccagctgg2040 tgccagactt ttggtgctaa ggcctgcaag gggcctgggg cagtgcgtat tctcttccct2100 ctgacctgtg ctcagggctg gctctttagc aatgcgctca gcccaatttg agaaccgcct2160 totgattoaa gaggotgaat toagaggtoa cotottoato coatoagoto coagactgat2220 gccagcacca ggactggagg gagaagcgcc tcaccccttc ccttccttct ttccaggccc2280 ttagtcttgc caaaccccag ctggtggcct ttcagtgcca ttgacactgc ccaagaatgt2340 ccaggggcaa aggagggatg atacagagtt cagcccgttc tgcctccata gctgtgggca2400 ccccagtgcc taccttagaa aggggcttca ggaagggatg tgctgtttcc ctctacgtgc2460 ccagtectag cetegeteta ggacccaggg etggetteta agttteegte cagtetteag2520 gcaagttctg tgttagtcat gcacacacat acctatgaaa ccttggagtt tacaaagaat2580 tgccccagct ctgggcaccc tggccaccct ggtccttgga tccccttcgt cccacctggt2640 ccaccccaga tgctgaggat gggggagctc aggcggggcc tctgctttgg ggatgggaat2700 gtgtttttct cccaaacttg tttttatagc tctgcttgaa gggctgggag atgaggtggg2760 totggatott ttotcagago gtotccatgo tatggttgca tttccgtttt ctatgaatga2820 atttgcattc aataaacaac cagactcaga taaaaaaaaa

(2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2137 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

gtccgctttc	gtctccgtcd	tgctgccgtt	accgccgctg	g ctgccgccgc	ttgcgtcccc	60
cgctccggt	: tgtggtgcag	g ccgggaccca	ggaccatgto	: tctgtctcac	tcagaggaga	120
tgcaccggct	: cacggaaaat	: gtctataaga	ccatcatgga	gcagttcaac	cctagectee	180
ggaacttcat	cgccatgggg	, aagaattaco	agaaggcact	gacaaatata	. acatataa	240
	· ceregacyce	, urygrqaaqa	tadadaaact	. aaccaacaac	20000000-	
	. cygagacyci	. Cttttccada	. taactaaaat	. CC3C3CGC3C	, ataaa	300
agorggaago	. aatgetgaag	luttucaca	accadetoct	' tacqcaqctq	G3GG3G3G-	360
tggagctgga	ctccaggtat	ctgagtgctg	cactaaaaaa	ataccadact	gagcagaagg	420
gcaaaggcga	cgccctggac	aagtgtcagg	ctgagetgaa	gaagettegg	aagaagagcc	480
agggcagcaa	gaatcctcag	aagtactcgg	acaaggagct	GCagtacato	gacgccatca	540
gcaacaagca	gggcgagctg	gagaattacg	tatccaacaa	: gtagtatatt	gacyccatca gcactgacag	600
aggagcgcag	gcgcttctqc	ttcctaataa	agaagcagtg	Caccatage	aagaactccg	660
cggcctacca	ctccaagggc	aaggagetge	taacacaaaa	actacaata	tggcaacagg	720
cctgtgccga	ccccagcaag	atcccggagc	acacaataca	getgetgetg	caggtggcca	780
gcaacggcgc	caccctcccc	aggggggtgt	Caacataa	gttcatgcag	gtcatttccg	840
accccattcc	gggggcaag	CCCtaccaa	tocccccaa	gcccaacctg	ttcgtggggc	900
ggatgtctgc	ccaggagagc	acacccatca	tgaacggcgt	gerggeadeg	gatggcgagg1	960
actacagece	gtgggctgac	Cacaaaacta	CCCacccca	cacaggeeeg	gatggcgaggl	.020
ctcagagcaa	gctcagcgac	tectacteca	acacactece	acceetgtet	cctccgcagt1	.080
caaaaaacag	ctatoccacc	accoadaaca	acacactece	tacataca	agcgtgacccl	140
ccaacctaga	gcgcaatggc	catatacaaa	tgaagggat	ctgctcgagc	tccatggcag1 gctgctgggg1	200
acaacagcac	cctcctgage	ttcaaggagg	ataaceteat	tagatast	gctgctggggl gtgcctgaggl	260
cccgcgatgg	ctggcactac	agagagagta	agaagagaga	cateetgetg	gtgcctgaggl	320
tctcctacac	ccaaatctta	gacagcgatg	agaagaccaa	gatgegggge	tggtttccct1 agcctgcagc1	380
aagggaagag	cagcagcacg	ggcaacctcc	tagacaa	gergeacatg	agcctgcagcl atcccaccccl	440
ccgattacgg	caccacctcc	caaacttcc	cogacaagga	cyacctggcc	atcccaccccl	500
ggccctacag	tataaccata	cccaccttct	ccgcccagac	ggccagcggc	ttcaagcaga1	560
ccatgagcag	caccastata	gaagtggcca	gattetease	ggatgactat	ggagcgcggt1	620
ccctttaccc	acqtccaqct	gaageggeea	gtgaggg	egeetgaeta	gagttagaat1	680
agctgatggc	cacatotoca	gtagtagaca	totactact	acaggtctgc	cccctcctc1	740
acctattcta	tcatcatctc	tacattacta	totagigget	tececegee	ttcccatgtal	800
atcttaccc	acttgagtct	agestagest	ryragagaac	atccaggccc	cggctgcctgl	860
agagtgggg	gcaggccct	gaaggggact	accorates	tgttctaggc	agggccgggc1	920
gaccacctct	tgagggtaca	cacctctact	account age	raggetgeee	agggccgggc1	980
agttaaggga	ggacatttgg	ccarctagt	catacaggeea	rggagccttg	ggtacccctg2	J40
ttctcctacc	taataaacag	gcttctcctg	gurgggaggg	gageetgget	gccctgctgc2	100
		· ·	cadadaa		2:	137

(2) INFORMATION ON SEQ ID NO. 43:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2410 base pairs

 - (B) TYPE: Nucleic acid(C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

	ttgagcagac	acaggtgcag	, gcagtggtga	ctctacaggo	cctgctattc	cgggcccttt	60
	igcaacgitg	tggcaacaat	: aaaattttga	cgtagccatc	: ctccatttgg	aagtotagta	120
	gerggerege	cycygaaatg	, accetgitt	tatttccaga	attacctcto	ggtttägaga	180
	agiggitti	aaacgagigi	. gggtaaaaaa	: aattacctga	ggtacttgtc	agagtcgcag	240
	acticiaggi	cccacccago	cctcatcaat	cagtttagtg	, agggtggtgc	ccaggactct	300
	gactitaaac	atacccctag	aaagattctg	atacaggtag	. aggtgagaag	ccctaattta	360
	gaggcagccc	ggeeteeett	catggtggga	ccaqqqccaq	cagggaatgt	Caggggggacc	420
	Colyacolle	accycgaett	ctggcttgca	gagggtggcc	cqqqaqqaqa	taataaaaa	480
	ageteaacag	cygyaaggcy	alglacgcct	tctgcagagt	gaaggacccc	aactctggac	540
	tycccaaatt	tgtcctcatc	aactggacag	gcgagggcgt	gaacgatgtg	COGGAGGGGGG	600
	cccgcgccag	ccacgccage	accatggcca	gcttcctqaa	gggggccat	gtgaccatca	660
	acgcacggge	cgaggaggat	grggagcctg	agtgcatcat	ggagaaggtg	gccaaggett	720
	caygigeeaa	ctacagettt	cacaaggaga	gtggccgctt	ccaggacgtg	ggaccccagg	780
	ccccagiggg	Cicigigiae	cagaagacca	atgccgtgtc	tgagattaaa	agggttggta	840
	aayacagctt	ctgggccaaa	gcagagaagg	aggaggagaa	ccatcaacta	gaggaaaagc	900
	ggcgggccga	ggaggcacag	cggcagtgga	gcaggagcgc	caaaacata	agtgcgtgag	960
	gergeacgee	gggagcagcg	ctatcaggag	cagggtggcg	aggccagccc	Ccagaggacg1	020
	Çgggagcagc	agcaagaagt	ggtttcaagg	aaccgaaatg	agcaggagtc	taccatacac1	080
	ccyaygyaya	ttttcaagca	gaaggagagg	gccatgtcca	ccacctccat	ctccagtcct1	140
	cagcciggca	agcigaggag	ccccttcctg	cagaagcagc	tcacccaacc	agagacccac1	200
	reigglagag	agecageege	tgccatctca	aggcccaggg	cagatetece	tactagagag1	260
	ccggcgccca	geacteetee	atgtctggtg	caggcagaag	aggaggctgt	gtatgaggaa1	320
	ccccagage	aggagaeeee	ctacgagcag	ccccactgg	tqcaqcaqca	aggtgctggc1	380
	icigagcaca	Ligaccacca	cattcagggc	caggggctca	gtgggcaagg	getetatace1	440
	cgcgccccgc	acgactacca	ggcagccgac	gacacagaga	tctcctttga	CCCCGagaac1	500
	ctcatcacgg	gcategaggt	gatcgacgaa	ggctggtggc	gtggctatgg	gccggatggc1	560
	caccccggca	rgridddige	caactacgtg	gageteattq	agtgaggctg	agggcacatc1	620
	cigacatata	CCCCCagac	arggerreer	tattgctgga	agaggaggcc	taggaattaa1	ഒമറ
	cattcaycat	tetteeagga	ataggacccc	cagtgaggat	gaggeeteag	ggetecetec1	740
	ggcttggcag	actcagcctg	tcaccccaaa	tgcagcaatg	gcctggtgat	tcccacacat1	ลกก
	cccccccgca	redeedgaee	ctcccagaca	gcttggctct	tgcccctgac	aggatactgal	860
•	gccaagccct	gcctgtggcc	aagccctgag	tggccactgc	caagctgcgg	ggaagggtccl	920
•	tgagcagggg	catctgggag	gctctggctg	ccttctgcat	ttatttgcct	tttttcttt1	980
1	tctcttgctt	ctaaggggtg	gtggccacca	ctgtttagaa	tgacccttgg	gaacagtgaa2	040
(cgtagagaat	tgtttttagc	agagtttgtq	accaaagtca	gagtggatca	tggtggtttg2	100
(gcagcaggga	atttgtcttg	ttggagcctg	ctctatactc	cccactccat	ttctctgtcc2	160
(ctctgcctgg	gctatgggaa	gtggggatgc	agatggccaa	gctcccaccc	tgggtattca2	220
ė	aaaacggcag	acacaacatg	ttcctccacq	cggctcactc	gatgcctgca	ggccccagtg2	280
•	rycyccicaa	Cigalicitga	cttcaggaaa	agtaacacag	agtggccttg'	acctattate2	310
ŧ	tcccctatt	ttctgtccca	gctcatccgt	gtctctgaag	aacaaatata	cttttggacc2	100
ä	aaaaaaaa		-			2.000090002	110
						. 2.	3 T U

(2) INFORMATION ON SEQ ID NO. 44:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2333 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
tgaaaaatgc ggacagtata ttcagaaagg ctattccaag ctcaagatat ataattgtga
actagaaaat gtagcagaat ttgagggcct gacagacttc tcagatacgt tcaagttgta 120
ccgaggcaag tcggatgaaa atgaagatcc ttctgtggtt ggagagttta agggctcctt 180
teggatetae cetetgeegg atgaceceag egtgeeagee ceteceagae agttteggga 240
attacctgac agcgtcccac aggaatgcac ggttaggatt tacattgttc gaggcttaga 300
gctccagccc caggacaaca atggcctgtg tgacccttac ataaaaataa cactgggcaa 360
aaaagtcatt gaagaccgag atcactacat tcccaacact ctcaacccag tctttggcag 420
gatgtacgaa ctgagctgct acttacctca agaaaaagac ctgaaaattt ctgtctatga 480
ttatgacacc tttacccggg atgaaaaagt aggagaaaca attattgatc tggaaaaccg 540
attectttee egetttgggt eecactgegg cataceagag gagtactgtg tttetggagt 600
caatacetgg egagateaae tgagaeeaae acagetgett caaaatgteg eeagatteaa 660
aggetteeca caacceatee ttteegaaga tgggagtaga ateagatatg gaggaegaga 720
ctacagettg gatgaatttg aagccaacaa aatcetgeac cagcaceteg gggeeeetga 780
agageggett getetteaca teeteaggae teaggggetg gteeetgage aegtggaaac 840
aaggactttg cacagcacct tecageceaa cattteecag ggaaaactte agatgtgggt 900
ggatgttttc cccaagagtt tggggccacc aggccctcct ttcaacatca caccccggaa 960
agccaagaaa tactacctgc gtgtgatcat ctggaacacc aaggacgtta tcttggacga1020
gaaaagcatc acaggagagg aaatgagtga catctacgtc aaaggctgga ttcctggcaa1080
tgaagaaaac aaacagaaaa cagatgtcca ttacagatct ttggatggtg aagggaattt1140
taactggcga tttgttttcc cgtttgacta ccttccagcc gaacaactct gtatcgttgc1200
gaaaaaagag catttctgga gtattgacca aacggaattt cgaatcccac ccaggctgat1260
cattcagata tgggacaatg acaagttttc tctggatgac tacttgggtt tcctagaact1320
tgacttgcgt cacacgatca ttcctgcaaa atcaccagag aaatgcaggt tggacatgat1380
teeggacete aaageeatga acceeettaa ageeaagaca geeteeetet ttgageagaa1440
gtccatgaaa ggatggtggc catgctacgc agagaaagat ggcgcccgcg taatggctgg1500
gaaagtggag atgacattgg aaatcctcaa cgagaaggag gccgacgaga ggccagccgg1560
gaaggggggg gacgaaccca acatgaaccc caagctggac ttaccaaatc gaccagaaac1620
ctccttcctc tggttcacca acccatgcaa gaccatgaag ttcatcgtgt ggcgccgctt1680
taagtgggtc atcatcggct tgctgttcct gcttatcctg ctgctcttcg tggccgtgct1740
cctctactct ttgccgaact atttgtcaat gaagattgta aagccaaatg tgtaacaaag1800
gcaaaggett catttcaaga gtcatccage aatgagagaa teetgeetet gtagaccaac1860
atccagtgtg attttgtgtc tgagaccaca ccccagtagc aggttacgcc atgtcaccga1920
gccccattga ttcccagagg gtcttagtcc tggaaagtca ggccaacaag caacgtttgc1980
atcatgttat ctcttaagta ttaaaagttt tattttctaa agtttaaatc atgtttttca2040
aaatattttt caaggtggct ggttccattt aaaaatcatc tttttatatg tgtcttcggt2100
tctagacttc agcttttgga aattgctaaa tagaattcaa aaatctctgc atcctgaggt2160
gatatactic atattigtaa tcaactgaaa gagctgtgca ttataaaatc agttagaata2220
gttagaacaa ttcttattta tgcccacaac cattgctata ttttgtatgg atgtcataaa2280
agtctattta acctctgtaa tgaaactaaa taaaaatgtt tcacctttaa aac
```

(2) INFORMATION ON SEQ ID NO. 45:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1612 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
gtettetttt ttttetttt tttttttt ttttttttc eetgtggaag tgettttatt 60
agcagtaagg ctgatcgtac aaaaaattct cagagcttca taggacaagg tagtacaagt 120
atggatgata caggactgag gaacggggga cggctcaaaa gaaatcaaca tcgtctgggg 180
catccaggtc ccgatattcc acaatggccc ttgggtctcc acgaaccatc ctgttgcgag 240
gtttcccagg ataacctccc tggcctcgga aggcatcata gttccctcga ccagcaccat 300
acggggcatg ggggtatgga gggcctcctg tggggactgc agggcggaca gcaccagctc 360
catageceaa gateggggge eggggetgae catagggeat eaggeeetgg ggagtetggt 420
gtgggtaggg gagtcctggg gtcaaacctg gggggagtat ctgggcgggc ccaggtggct 480
gggctggctt gatctcaggc agagctgggc gcttagcatc agtgaggaag ttgttaaaaa 540
acgcgacttc ctttttcact tcctcaattt tctctgcatg cttgttgaag atatgtttgc 600
gcacaaactc aggacccttg aatttcttgc cactgagagg acacagccac ttatccttgc 660
ccagttcctg cgtgttggag gtgacgaact tctccacttc ctgctctggg tctttgcgcc 720
ccatcttctg ggcctcttcc tctgagagtg actcccgcac actcagcaac ggcgtgagct 780
tetecteaaa agtettetge eacteeagea etteeeegtg aetgatgegg ttgggtggea 840
tgggcccccg aacgtggatg atcccacage gattgggcat ctcgtcctcg ttggggtact 900
cacaggtgtt gtaataatcc aaggaatgca cgatgcgcag gtaaaggagg agcttgtcca 960
agacettaat caacttetea teeegeteea egttgatete tgeegggtte cetteettag1020
gaggeteete aggaggageg ceeeegetge teeecageag eteeteetee teggegetta1080
cttcctcgat caggtagtcg gtgatattct tcaagatcgg gttttgcgag ggcaggctcg1140
tgggcagggg aggcgtccct ggttctgagg cccaaagctg tgtcctgtca tccagcgtgt1200
ggatcagett ggeegeeage ttgatgtegt tgegeaeaat etgettgtge tgggtgatge1260
cgttgatgtt gcgaacgcgc cgggtcaggt ccctgttcac accagggctc agctcacact1320
cccggagacg gatgttctgc aggttccaac agatctcttt aatgttaaca ctgcggtcgal380
aggtcaccca gccacgacgg aaaaacctcc tctctggctg gggctctgag agcgccaccc1440
gcataaagcc tgggtacctt ttacaaaggg agatgatctc ggcccgggag atgttgggcg1500
cgatgttgcg catgaagagg gagcaggtct tatgcagcgg ccgcqgcttg cactccaqcc1560
coggogote cttgggctte teccattett ettecttggg etteteette te
```

- (2) INFORMATION ON SEQ ID NO. 46:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1106 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
gaaagetetg gettteagge tataggaaga geagaagatg atgeeagaag ttgetgggtt 60
aaaaccagcg agtccacccg tecttaccag etectcagaa ggeggagace gaccetgata 120
acttaccgga tatttcgtca cagaagacac aaagacacat ccagcgggga ccacctcacc 180
tgcagattag acccccaagc caaagacctg aaggatggga cccaggagga ggccacaaaa 240
aggcaagaag cccctgtgga tccccgcccg gaaggagatc cgcagaggac agtcatcagc 300
tggagggag cggtgatcga gcctgagcag ggcaccgagc tcccttcaag aaqagcagaa 360
gtgcccacca agcctcccct gccaccggcc aggacacagg gcacaccagt gcatctgaac 420
tatcgccaga agggcgtgat tgacgtcttc ctgcatgcat ggaaaggata ccgcaagttt 480
gcatggggcc atgacgagct gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc 540
ggtctcacac tgatcgacgc gctggacacc atgtggatct tgggtctgag gaaagaattt 600
gaggaagcca ggaagtgggt gtcgaagaag ttacactttg aaaaggacgt ggacgtcaac 660
ctgtttgaga gcacgatccg catcctgggg gggctcctga gtgcctacca cctgtctggg 720
gacageetet teetgaggaa agetgaggat tttggaaate ggetaatgee tgeetteaga 780
acaccatcca agattcctta ctcggatgtg aacatcggta ctggagttgc ccacccgcca 840
cggtggacct ccgacagcac tgtggccgag gtgaccagca ttcagctgga gttccgggag 900
ctctcccgtc tcacagggga taagaagttt caggaggcag tggagaaggt gacacagcac 960
atccacggcc tgtctgggaa gaaggatggg ctggtgccca tgttcatcaa tacccacagt1020
gggcctgttt cacccacctg gggcgtattt cacggtgggg cgccaggggc cgacagctta1080
ttattgagtt acctgtttga aaggca
```

(2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1370 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
geggtggega ggggegtaac ggttgttgta gteeggeeee eteetggetg gteeageeae
attaaccggc aggatgtcgg aggtgcggct gccaccgcta cgcgccctgg acgactttgt 120
tetggggteg gegegtetgg eggeteegga tecatgegae eegeagegat ggtgeeaeeg 180
egteateaac aaceteetet actaceaaac caactacett etetgetteg geateggeet 240
egetetegee gggtaegtge ggceaettea taegeteetg agegegetgg tagtggeggt 300
ggccctcggc gtgctggtgt gggcagctga gacccgcgca ctgtgcgccg ctgccqccgc 360
agccaccetg cagectgeet ggeogeagtg ettgeogteg geotectggt getetgggte 420
gegggeggeg ettgeacett cetgtteage ategeeggge eggtgettet gateetggtg 480
cacgcctcgt tgcgcctgcg caaccttaag aacaagattg agaacaagat cgagagcatt 540
ggtctcaagc ggacgccaat gggcctgcta ctagaggcac tgggacaaga gcaggaggct 600
ggatcctagg cccctgggat ctgtacccag gacctggaga ataccaccc accccagcc 660
cataattggg acccagagee ettteccage acttaaaaca ggageetaga geeeeetgee 720
caaacaaaac aggacatctg tgaccgccct acccccacgc cagccccaaa ctaagatatc 780
cctcacaccc agcccccatt acctagggac aagagtcttc cccagccttg aacctaggac 840
caaqagccac ctacatccag ccccaaaact ggggcttcag gccagagcat ccatggccaa 900
tttcaaattg tgaacccaga gacactccca tccacccttc tccatgctca tccccaaact 960
ggggcctgga gcaaggcact ctcaaatctt gaaccctgga ccaaagcttt tccagacccc1020
accetacett ccaacccagg tcaagacatt gccaaatett gaactcagaa cccaagtgtt1080
ccatgcccct gtgtggatgg agtcgggtat cctgactgtt ggacccctgg tccaqqtgat1140
cccgaccctc accagtccca tttgcctccc tccagctctg cttaggcatt ttgcccctcal200
ccccaatgtt ccacaccatc gacaaccaag gggtgaggtg gggacaggcc tcagcaggga1260
atggggcgta tatgttagtg ttgctgcaac aataaagcct gttgcatctc tcatgccaaa1320
aaaaaaaaa aagtcgaccg gccgcaaata tagtagtagt agtcgtccgc
```

- (2) INFORMATION ON SEQ ID NO. 48:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ctcgtagtt attaaatgat gtacaatttg gccagtttgg agatgacca aaggaggaag 60 taatggttct ggagagaatc ttactggcag accatcaagg ttgatttaca ggtagaacat120 ccataccagt tcctactaaa atatgcaaag caactcaaag gtgataaaaa caaaattcaa180 aagttggttc aaatggcatg gacatttgta aatgacagtc tctgcaccac cttgtcactg240 cagtgggaac cagagatcat agcagtagca gtgatgtatc tcgcaggacg tttgtgcaaa300 tttgaaatac aagaatggac ctccaaaccc atgtatagga gatggtgga gcagtttgtt360 caaggaagac aacagatgcc tcatcacac ccccatcagc tgcaacagc tcttactca420 caaggaaaac aacagatgcc tcggccctgt ggttgctggg cctccca ccccgctgcc tgggccctgt ggttgctggg cctccaaa accaagaggg540 aaggttgtac agcccgaacc cgtggagcaa tgccctgtct ggcctccaa accaaaataa600 aactgggtca ctttaaa

- (2) INFORMATION ON SEQ ID NO. 49:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1899 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
tgtgtgaggc ccaacagcgg aatcatcgat gcaggggcct gaattaatgt atctgtgatg
ttacagcctt tcgattatga tcccaatgag aaaagtaaac acaggttatg gttcagtcta 120
tgtttgctcc aactgacact tcagatatgg aagcagtatg gaaggaggca aaaccggaag 180
accttatgga ttcaaaactt agatgtgtgt ttgaattgcc agcagagaat gataaaccac 240
atgatgtaga aataaataaa attatatcca caactgcatc aaagacagaa acaccaatag 300
tgtctaagtc tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag ttcaaggaag 420
aagatggact gcggatgagg aagacagtgc agagcaacag ccccatttca gcattagccc 480
caactgggaa ggaagaaggc cttagcaccc ggctcttggc tctggtggtt ttgttcttta 540
tcgttggtgt aattattggg aagattgcct tgtagaggta gcatgcacag gatggtaaat 600
tggattggtg gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 660
aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc ctgcacacac 720
atacacagat acacacaca aaatataatg taacgatctt ttagaaagtt aaaaatgtat 780
agtaactgat tgagggggaa aagaatgatc tttattaatg acaagggaaa ccatgagtaa 840
tgccacaatg gcatattgta aatgtcattt taaacattgg taggccttgg tacatgatgc 900
tggattacct ctcttaaaat gacacccttc ctcgcctgtt ggtgctggcc cttggggagc 960
tggagcccag catgctgggg agtgcggtca gctccacaca gtagtcccca cgtggcccac1020
teceggeeca ggetgettte egtgtettea gttetgteea agecateage teettqqqae1080
tgatgaacag agtcagaagc ccaaaggaat tgcactgtgg cagcatcaga cgtactcgtc1140
ataagtgaga ggcgtgtgtt gactgattga cccagcgctt tggaaataaa tggcagtgct1200
ttgttcactt aaagggacca agctaaattt gtattggttc atgtagtgaa gtcaaactgt1260
tattcagaga tgtttaatgc atatttaact tatttaatgt atttcatctc atgttttctt1320
attgtcacaa gagtacagtt aatgctgcgt gctgctgaac tctgttgggt gaactggtat1380
tgctgctgga gggctgtggg ctcctctgtc tctggagagt ctggtcatgt ggaggtgggg1440
tttattggga tgctggagaa gagctgccag gaagtgtttt ttctgggtca gtaaataaca1500
actgtcatag ggagggaaat tctcagtagt gacagtcaac tctaggttac cttttttaat1560
gaagagtagt cagtottota gattgttott ataccacoto toaaccatta otcacacttc1620
cagcgcccag gtccaagtct gagcctgacc tccccttggg gacctagcct ggagtcagga1680
caaatggatc gggctgcaga gggttagaag cgagggcacc agcagttgtg ggtggggagc1740
aagggaagag agaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga1800
attaatttta tgccataaaa gaccaaccca gttctgtttg actatgtagc atcttgaaaa1860
gaaaaattat aataaagccc caaaattaag aaataaaaa
                                                                 1899
```

(2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1398 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

agaatgtcgg gcggtgctgc gaggcccaag cccgggccgg ggccgcctcc ctcaacgcct 60 ccettqacqq cctccacaac gcactcttcq ccactcagcq cagcttggag cagcaccagc 120 ggctcttcca cagcctcttt gggaacttcc aagggctcat ggaagccaac gtcagcctgg 180 acctggggaa gctgcagacc atgctgagca ggaaagggaa gaagcagcag aaagacctgg 240 aagctccccg gaagagggac aagaaggaag cggagccttt ggtggacata cgggtcacag 300 ggcctgtgcc aggtgccttg ggcgcggcgc tctgggaggc aggatcccct gtggccttct 360 atgccagett ttcagaaggg acggetgeee tgcagacagt gaagttcaac accacataca 420 tcaacattgg cagcagctac ttccctgaac atggctactt ccgagcccct gagcgtggtg 480 tctacctgtt tgcagtgagc gttgaatttg gcccagggcc aggcaccggg cagctggtgt 540 ttggaggtca ccatcggact ccagtctgta ccactgggca ggggagtgga agcacagcaa 600 cggtctttgc catggctgag ctgcagaagg gtgagcgagt atggtttgag ttaacccagg 660 gatcaataac aaagagaagc ctgtcgggca ctgcatttgg gggcttcctg atgtttaaga 720 cctgaaccc agccccaatc tgatcagaca tcatggactc gcccagctct cctcggcctg 780 gggctctggc caaggatggg ctggaggtca ttcagttggt ctgtctcttc cctggaaacc 840 ttctgcaaag atggtgtgt gtacgtggct tccctgtaac cacatggggc ttggccattt 900 ctccatgatg agaaggactg gaatgettet eegggeagga catggteeta ggaageetga 960 accttggctt ggcatgcctt ctcagacage acggcctggg ctccaactct tcaccacacc1020 ctgtattcta caacttcttt ggtgttttgc tcctcctgtg gttggaaact tctgtacaac1080 actttaaact tttctcttgc ttcctcttct cttctccctt atcgtatgat agaaagacat1140 tcttccccag gaggaatgtt taaaatggag gcaacatttt ggccaacatt ggaaagcact1200 agagggcaat gggattaaac caacctgctt ggtctctatt agtcagtaat gaagacgaca1260 gcctggccaa ccaagggaaa ggaaattagt atctttagtt tcagtcattc cttgtagggg1320 tatgggtttt agcttgtggc ccccaccgaa aagattcatc ttggattgtt aatgcctatt1380 1398 attccccaca ttaagggg

(2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1340 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
tttggcatca tttacaattt catagaatta ctgtgaaggc ctttctagtt gagatgttgg 60
ggtatttggg attctaattg ttaaccccag aagaaggtaa tttagcttgt atttatttaa 120
aacccattta qccttttact tatatctggt agaattccag tgatcatcct aataaggtat 180
atttcagaat aattttttt tccttcagaa taacttagaa tcagatgcta taagggctcc 240
taggagcagt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatatta 300
aaccaaqaqq ccatttccaa tatgattttt tgtttctttt taacttgtta aqtccctaaq 360
agattacatg ctagggcttg agtcatttct attgtagata atgatggccc acacagtcac 420
cttcaactat ccacataagc taggctttcc gcttttgcca cggacagtgt gaccaagata 480
tttccagagt aaataaccca ccacaacctt ggtaattcct cttttcttct taagctccag 540
gaagcgaaag cagaaggact cttttcagac tgccctctgt agcctacatt gcagctttcc 600
aaaacaggca gctagcactg ggaaagccca tgtggtgacc ccatattttt ctgaggttct 660
tcttttccat ggtgttactt tattatcaga aagtaaattc agaaaacagg tcttgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tccagcccca gaacttgtaa ggattttgtt tgaacactga gcagatgcct 840
cctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ttgccttcac agagtcctcc ttgacacccc tgacttaatg atagttgctg ttttggagta1020
gaattgatca ggtttaagtc atcctgctca ggttgggcat agtggctcat gcctgtaatc1080
tcagcacttt gggaagccaa agtgggagga ttgcttgagc ccaggagttc caaaccatccl140
tgggcaacag agggagaccc tgtctctacc aagaaaaaaa aaaaaaaaa aaagttaaaa1200
aaacaattag ctggacctgg tggtgcacac tcagtaggct gaggtgaaag gattcctttal260
acatgggaga ctgaagatgc agtgagccat gaatcagcaa ctgcacacca gtatgagaga1320
aaaagtggaa ccctatcaca
```

- (2) INFORMATION ON SEQ ID NO. 52:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

atcagcacat caattgcagc attgtggcta ccagggggtc aggatgcggg cggtggagcc 60 ctctggcctt tgtgtggtag ccgaggactc tgtgtcagcg accgttttcc gggaaacttc120 cgggcgagac tcacatcttg gaaattcaaa tactcaatag ctctcgaatt ctaggaatct180 tgagaagagg cctggattaa ggattcagac gtgggccctc agatggctat ggcattgctg240 gttctaccaa cgtgacaggt gatcaagtta agaagctgga cgtcctctcc aacgacctgg300 gtatggaaca ggtta

- (2) INFORMATION ON SEQ ID NO. 53:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1162 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
eggetegage ggetegagat tegaggtegt ggtggtettg gaagagegte gagggggeeg
tggacgtgga atgggccgag gagatggatt tgattctcgt ggcaaacgtg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaacgtggag gtagcggatc 180
tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaataca ttcagaaaca 240
aatatettat aattacagtg aettggatea ateaaatgtg aetgaggaaa eacetgaagg 300
tgaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgagtggaag gctattcaaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtggaagaa 480°
gggatttgtt cttcataaat caaagagtga agaggctcat gctgaagatt cggttatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttggaga 600
cettggccgc ccaggacgtg gcggcagggg aggacgaggt ggacgtgggc gtggtgggcg 660
cccaaaccgt ggcagcagga ccgacaagtc aagtgcttct gctcctgatg tggatgaccc 720
agaggcattc ccagctctgg cttaactgga tgccataaga caaccctggt tcctttgtga 780
accettetgt teaaagettt tgeatgetta aggatteeaa acgaetaaga aattaaaaaa 840
aaaaagactg tcattcatac cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat ttagaaatgt 960
attggtagca gggatgtttt cataattttc agagattatg cattcttcat gaatactttt1020
gtattgctgc ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac1080
cagttaaaaa aatcacaaaa aaaaaaaatt ttaattaagg atttagaagt tcccccaatt1140
acaaactggt tttaaatatt gg
```

- (2) INFORMATION ON SEQ ID NO. 54:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1826 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

cggctcgagg	ccccgccct	gttcgccccg	cgccaccggc	ccgcgccccg	ccatggagga 60
cctggatgcc	ctgctctctg	acctggagac	taccacctcg	cacatgccaa	ggtcaggggc 120
tcccaaagag	cgccctgcgg	agcctctcac	ccctccccca	tcctatggcc	accagccaca 180
gacagggtct	ggggagtctt	caggagcctc	gggggacaag	gaccacctgt	acagcacggt 240
atgcaagcct	cggtccccaa	agcctgcagc	cccggcggcc	cctccattct	cctcttccag 300
cggtgtcttg	ggtaccgggc	tctgtgagct	agatcggttg	cttcaggaac	ttaatgccac 360
tcagttcaac	atcacagatg	aaatcatgtc	tcagttccca	tctagcaagg	tggcttcagg 420
agagcagaag	gaggaccagt	ctgaagataa	gaaaagaccc	agcctccctt	ccagcccgtc 480
tcctggcctc	ccaaaggctt	ctgccacctc	agccactctg	gagctggata	gactgatggc 540
ctcactctct	gacttccgcg	ttcaaaacca	tcttccagcc	tctgggccaa	ctcagccacc 600
ggtggtgagc	tccacaaatg	agggctcccc	atccccacca	gagccgactg	gcaagggcag 660
cctagacacc	atgctggggc	tgctgcagtc	cgacctcagc	cgccggggtg	ttcccaccca 720
ggccaaaggc	ctctgtggct	cctgcaataa	acctattgct	gggcaagtgg	tgacggctct 780
gggccgcgcc	tggcaccccg	agcacttcgt	ttgcggaggc	tgttccaccg	ccctgggagg 840
cagcagcttc	ttcgagaagg	atggagcccc	cttctgcccc	gagtgctact	ttgagcgctt 900
ctcgccaaga	tgtggcttct	gcaaccagcc	catccgacac	aagatggtga	ccgccttggg 960
cactcactgg	cacccagagc	atttctgctg	cgtcagttgc	ggggagccct	tcggagatga1020
gggtttccac	gagcgcgagg	gccgccccta	ctgccgccgg	gacttcctgc	agctgttcgc1080
cccgcgctgc	cagggctgcc	agggccccat	cctggataac	tacatctcgg	cgctcagcgc1140
gctctggcac	ccggactgtt	tcgtctgcag	ggaatgcttc	gcgcccttct	cgggaggcag1200
ctttttcgag	caçgagggcc	gcccgttgtg	cgagaaccac	ttccacgcac	gacgcggctc1260
gctgtgcgcc	acgtgtggcc	tccctgtgac	cggccgctgc	gtgtcggccc	tgggtcgccg1320
cttccacccg	gaccacttca	catgcacctt	ctgcctgcgc	ccgctcacca	aggggtcctt1380
ccaggagcgc	gccggcaagc	cctactgcca	gccctgcttc	ctgaagctct	tcggctgaca1440
gcccgctcgg	ctcgccctct	ccccggagg	ccgcgccctc	ccggaaaagc	cgggtcctcc1500
agaccccgag	gccttgctct	cagagcggga	ggccccaccc	actggagagc	cccgccccta1560
aggtactatg	agtcctcagg	ggtcaagttc	agaaacggcc	cagccagacc	taaacccaca1620
cgcccacaaa	gtggattgca	cacagacaag	aactcccgtg	cgggcctcca	ctctattccc1680
accettgagg	gageceett	actgggggag	ggtccttgca	attccagcga	atcggaggcc1740
aggccaggac	gtccttgctc	cctgcaccct	cactgttctg	tgcacttttt	ctacctacat1800
aaacacacgc	attccacctc	aaaaa		•	1826

- (2) INFORMATION ON SEQ ID NO. 55:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1114 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

gatgaagtag atgactttga ggacttcatc ttcagccact tctttggaga caaagcactg 60 aagaagaggt cagggaagaa ggacaagcac tcacagagcc caagagctgc ggggcccagg 120 gaggggcaca gcataggggg ctgacaccct gccccacagg gaatggcctt ggcctggccc 180 agcccaagat cccagcgtta tctaactcct ggagggtgga ctctgtcctg gcttgtttgg 240 tgtcctcaga tatctttcac acagtagage aaaatcacca gccctgcact gatgtcactt 300 tatgtagaaa aaggcottag ctggacotgo gttgoogtot atgcaaatgo atgcaaatac 360 tecaggeest gggatgtggg ettgtgtttt gteaetgtga agggggagat gggagaggag 420 cctgttttgg ggtggggtct ggggaaggca atctgattct gaagctaaag agctttcatc 480 ctcttgagtg tatgtcccca tagtgggccc cttgacccac atgctgaccg gtgccttggg 540 atttgactag agttgctggc tcgaggccca gcacgaggac ttaccctggg gttttgttag 600 gtttggaagc agctgtccct agggggtgaa gtccccccc ttttttttt tttacccctg 660 cttctcccac ggcttcacct ccctatgtga actgtagact cagatcccaa taaagtgctg 720 ttgcagctat gatgctaggt ggtttctaag cacaggggac accccacacc ccctgcctga 780 atggatgggt ccatcccagg cactggtact tgcccccttg ttctgtatcc ccctttgccc 840 ttgccttgcc cttccaacaa accctaggcc cttgagaagc tgatacttct ccttttgctc 900 acaqctqcct tqqccccacc cctqqqaqat qtaqcaaatt qaqtqtqqqt tttqqaqtct 960 qaqcctcagq ctcaaatcca ggccaagtga tcttgggcaa gttaatctct gggaactttg1020 qqtttcttat cctcaaaaaa qqcqatqqaa qqqctqqqqa aqtqattaaa taaaaqcaac1080 qcaagaaaaa aaaaaaaaaa aaaaaaaaaa aaaa

- (2) INFORMATION ON SEQ ID NO. 56:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1644 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```
ctcqaqccqt qcaaqtqqaa taacacgggc tgccaggccc tgcccagcca agaacgaagg 60
ccccagcaag gccttcgtga actgtgacga gaacagccgg cttgtctccc tgaccctgaa 120
cctggtgacc agggctgatg agggctggta ctggtgtgga gtgaagcagg gccacttcta 180
tggagagact gcagccgtct atgtggcagt tgaagagagg aaggcagcgg ggtcccgcga 240
tgtcagccta gcgaaggcag acgctgctcc tgatgagaag gtgctagact ctggttttcg 300
qqaqattqag aacaaaqcca ttcaggatcc caggcttttt gcagaggaaa aggcggtggc 360
agatacaaga gatcaagccg atgggagcag agcatctgtg gattccggca gctctgagga 420
acaaggtgga agctccagag cgctggtctc caccctggtg cccctgggcc tggtgctggc 480
agtgggagcc gtggctgtgg gggtggccag agcccggcac aggaagaacg tcgaccgagt 540
ttcaatcaga agctacagga cagacattag catgtcagac ttcgagaact ccagggaatt 600
tggagccaat gacaacatgg gagcctcttc gatcactcag gagacatccc tcggaggaaa 660
agaagagttt gttgccacca ctgagagcac cacagagacc aaagaaccca agaaggcaaa 720
aaggtcatcc aaggaggaag ccgagatggc ctacaaagac ttcctgctcc agtccagcac 780
cgtggccgcc gaggcccagg acggccccca ggaagcctag acggtgtcgc cgcctgctcc 840
ctgcacccat gacaatcacc ttcagaatca tgtcgatcct ggggccctca gctcctgggg 900
accecactee etgetetaac acctgeetag gttttteeta etgteeteag aggegtgetg 960
gtcccctcct cagtgacatc aaagcctggc ctaattgttc ctattgggga tgagggtggc1020
atgaggaggt cccacttgca acttctttct gttgagagaa cctcaggtac ggagaagaat1080
agaggtcctc atgggtccct tgaaggaaga gggaccaggg tgggagagct gattgcagaa1140
aggagagacg tgcagcgcc ctctgcaccc ttatcatggg atgtcaacag aatttttccc1200
tocactocat coctocctoc ogtocttocc ctcttcttct ttccttccat caaaagatgt1260
atttqaattc atactaqaat tcaggtgctt tgctagatgc tgtgacaggt atgccaccaal320
cactgctcac agcetttctq aggacaccag tgaaagaagc cacagctctt cttggcgtat1380
ttatactcac tgagtcttaa cttttcacca ggggtgctca cctctgcccc tattgggaga1440
ggtcataaaa tgtctcgagt cctaaggcct taggggtcat gtatgatgag catacacaca1500
ggtaattata aacccacatt cttaccattt cacacataag aaaattgagg tttggaagag1560
tgaagcgttt ttcttttct ttttttttt tgagacggag gtcttcactg tcgcccaggc1620
tggagtgcag tggcgcaatc tcgg
```

(2) INFORMATION ON SEQ ID NO. 57:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2184 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

	,					
tgcagtggtc	agagtgacct	ggtataaggg	agagggcatc	accttgcccc	ctgtgctgac	60
tcctgccctt	gtgcgagggg	agtccatccc	gatccggctc	ttcctggccg	ggtatgagct	120
cacgcccacc	atgcgggaca	tcaacaagaa	gttctctgtg	cgctattacc	tcaacctggt	180
gctgatagac	gaggaggagc	ggcgctactt	caagcagcag	gaagtggtgt	tgtggcggaa	240
		gcatgtccca				300
gggcaccacc	tccctgggtg	aggtgcggac	ccccagccag	ctgtctgaca	acaactgcag	360
gcagtaggcc	cccagggccg	agaagatgct	gggcacccac	ccagcacccc	catctaccaa	420
caccagegge	tgggggcggg	ggcggacctt	gtgaggctca	gttgacccgt	tacttgcaac	480
ctgaaaacaa	atcatgtttt	tgacttaaat	tcttttctct	ggagaaccca	aggggcttgg	540
		tgggattctg				600
ctggaagcca	gcctctctgg	ggaacatgag	ccccttcct	cggggggctg	ccttgcgtct	660
tagaggaggg	agagcagaga	gcacgcatcc	ttggctcctg	gctctctgag	cttcctgata	720
		gggattctga				780
					cccactaagt	
					gtggtgatct	
					cacctccctt	
					atggccttgg1	
gcacggagaa	gccctggggt	cagtgtcgtg	cacggatggc	ggcagtgttg	aacccaggag1	F080
					cacgtcgctc1	
					ccagcaagcc]	
					tgatccctcc1	
					gggaattggg1	
					tttacccctc1	
					cacacttccg1	
aatcattctg	cttgccaaat	aggtcatctt	caccagttga	ctgacccaag	tttaggacca1	1500
					cttgttatgc1	
					agtaaagttg1	
					attggcctcc1	
					atttggcagt]	
					ttcagttagt1	
					ttggcagggc1	
					agggcgactg1	
					gtgttcaggt1	
					gatcaaggtt2	
					agcatgaggt2	
			atattctaac	tagaagcatt	tgtcaagttc2	
cctgtgtggc	ccttccccc	agag			2	2184

(2) INFORMATION ON SEQ ID NO. 58:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1510 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
agcctgggaa acacagtagg gctccacctc tacaaaaaac acaaaaatta gccaggcatg
tggcgtcata gtagaattaa tcaaaagcaa gaaaatggct ggaggagctg tcttgttggc 120
aggacetect ggaactggca agacagetet ggetetgget attgeteagg agetgggtag 180
taaggtcccc ttctgcccaa tggtggggag tgaagtttac tcaactgaga tcaagaagac 240
agaggtgctg atggagaact teegeaggge cattgggetg egaataaagg agaccaagga 300
agtttatgaa ggtgaagtca cagagctaac teegtgtgag acagagaate ceatgggagg 360
atatggcaaa accattagcc atgtgatcat aggactcaaa acagccaaag gaaccaaaca 420
gttgaaactg gaccccagca tttttgaaag tttgcagaaa gagcgagtag aagctggaga 480
tgtgatttac attgaagcca acagtggggc cgtgaagagg cagggcaggt gtgataccta 540
tgccacagaa ttcgaccttg aagctgaaga gtatgtcccc ttgccaaaag gggatgtgca 600
caaaaagaaa gaaatcatcc aagatgtgac cttgcatgac ttggatgtgg ctaatgcgcg 660
gccccagggg ggacaagata tcctgtccat gatgggccag ctaatgaagc caaagaagac 720
agaaatcaca gacaaacttc gaggggagat taataaggtg gtgaacaagt acatcgacca 780
gggcattgct gagctggtcc cgggtgtgct gtttgttgat gaggtccaca tgctggacat 840
tgagtgcttc acctacctgc accgcgccct ggagtcttct atcgctccca tcgtcatctt 900
tgcatccaac cgaggcaact gtgtcatcag aggcactgag gacatcacat cccctcacgg 960
catecetett gacettetgg accgagtgat gataateegg accatgetgt atactecaca1020
ggaaatgaaa cagatcatta aaatccgtgc ccagacggaa ggaatcaaca tcagtgagga1080
ggcactgaac cacctggggg agattggcac caagaccaca ctgaggtact cagtgcagct1140
gctgaccccg gccaacttgc ttgctaaaat caacgggaag gacagcattg agaaagagca1200
tgtcgaagag atcagtgaac ttttctatga tgccaagtcc tccgccaaaa tcctgggctt1260
gaccaggcag ggataagtta cattgaagtt gagatggctt gagggttttt cagcagctaa1320
gagacttccc caggtgtgcc tggcctgggg tccagcctgt gggcgctttg ccctggggtt1380
tgggggctgc ccttccccat tcaggcgttg ggttgcagcg ttgttcaatt tcagttgttg1440
gaaagcgttt tttttttgaa gttagtctta agtgtttccc cttgggtttg ttttgaaaag1500
aacccttcct
                                                                 1510
```

(2) INFORMATION ON SEQ ID NO. 59:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1188 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
gagaactcac accatatgtg teetgtteea gtgegegggt etgtggagag eegggtgega
gcggcggcag cacgagggga aaagagctga gcggagacca aagtcagccg ggagacagtg 120
ggtctgtgag agaccgaata gaggggctgg ggccacgagc gccattgaca agcaatgggg 180
aagaaacaga aaaacaagag cgaagacagc accaaggatg acattgatct tgatgccttg 240
qctqcaqaaa taqaaqqaqc tggtgctgcc aaagaacagg agcctcaaaa gtcaaaaggg 300
aaaaagaaaa aagagaaaaa aaagcaggac tttgatgaag atgatatcct gaaagaactg 360
qaaqaattqt ctttgqaagc tcaaggcatc aaagctgaca gagaaactgt tgcagtgaag 420
ccaacagaaa acaatgaaga ggaattcacc tcaaaagata aaaaaaagaa aggacagaag 480
qqcaaaaaac aqaqttttga tgataatgat agcgaagaat tggaagataa agattcaaaa 540
tcaaaaaaga ctgcaaaacc gaaagtggaa atgtactctg ggagtttaac aaacttccta 600
aaaaagctaa agggaaagct caaaaatcaa ataagaagtg ggatgggtca gaggaggatg 660
aggataacag taaaaaaatt aaagagcgtt caagaataaa ttcttctggt gaaagtggtg 720
atgaatcaga tgaatttttg caatctagaa aaggacagaa aaaaaatcag aaaaacaagc 780
caggitectaa catagaaagi gggaatgaag atgatgaege eteetteaaa attaagaeag 840
tggcccaaaa gaaggcagaa aagaaggagc gcgagagaaa aaagcgagat gaagaaaaag 900°
cgaaactgcg gaagctgaaa gaaaaagaag agttagaaac aggtaaaaag gatcagagta 960
aacaaaagga atctcaaagg aaatttgaag aagaaactgt aaaatccaaa gtgactgttg1020
atactggagt aatteetgee tetgaagaga aageagagae teecacaget geagaagatg1080
acaatgaagg agacaaaaag aacgaaagat aagaagaaaa agaaaggagg acaagggagg1140
aaaaqaqaac aqaqaaqqaa aqaaqqqcct qqcaaaaqcc actgtttc
```

(2) INFORMATION ON SEQ ID NO. 60:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2208 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

gcaggacggc	tctaaaccct	tectooctoa	cttcaacggc	ttctcccacc	tggagctgag 60
					tcgtgttcct 120
					gcaaggggga 180
					tgggcaaggg 240
					gggtctcact 300
					tgttggggga 360
					ggggcgctcc 420
					gtgccatcca 480
					ggcaggtgga 540
					gcctcaatgg 600
					gattctcagg 660
					ccttggcctt 720
					aggcactgca 780
					tgctctggag 840
					ggcacctgca 900
					ccgtcaacac 960
					tgcaggtggg1020
caatgaggcc	cctgtgaccg	gctcctcccc	gctgggcgcc	acgcagctgg	acactgatgg1080
agccctgtgg	cttgggggcc	tgccggagct	gcccgtgggc	ccagcactgc	ccaaggcctal140
cggcacaggc	tttgtgggct	gcttgcggga	tgtggtggtg	ggccggcacc	cgctgcacct1200
gctggaggac	gccgtcacca	agccagagct	gcggccctgc	cccaccccat	gagctggcac1260
cagagccccg	cgcccgctgt	aattatttc	tatttttgta	aacttgtcgc	tttttgatat1320
					tccgtccagg1380
cagccgtgct	gcagacagac	ctagtgctga	gggatggaca	ggcgaggtgg	cagcgtggag1440
ggctcggcgt	ggatggcagc	ctcaggacac	acacccctgc	ctcaaggtgc	tgagccccg1500
					tcctgaatca1560
					aggtctgatg1620
					gctgctcctt1680
					ttccaaacaa1740
					ccaggctgct1800
					ggccctgccc1860
					ggggctatcg1920
					ctgggcctgg1980
					ggtctcatct2040
					cccacaaaag2100
					gcaagttttg2160
			aggttggaag		2208

- (2) INFORMATION ON SEQ ID NO. 61:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

gaaaaggggg agggggagtg acaatctttg cttggggcct atgacttctc cagccccaag 60 gggagatgcc accgggaaat cccccaatgt ccactagggg gcaggaggcc accgttcttc120 gtactccgga gaacctggct ggagagctct ttcttgttca cccttccctc cagctgtatc180 tctgccctgc agataacgtg aaggactgga gcaaggtcgt cctggcctat gagcctgtgt240 gggccattgg tactggcaag actgcaacac cccaacaggg aac 283

- (2) INFORMATION ON SEQ ID NO. 62:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

aacggaggat gcctaggctt ctggaggcga agaaggacgc ggcaagctgc gaaaagtcac 60 gggtatctgc aagcatgaaa tgatccgtga atatccgaat ggggcaaccc gtgcaggtga120 agcctgcaca cctgaataaa tcaggggcag acgcagggaa ctgaaacatc ttagtacctg180 cagg

- (2) INFORMATION ON SEQ ID NO. 63:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1780 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

tecceeceg gggcaacece eccateggge ecceaaageg etggggttac ageettaage 60 caccaagece eggeegacet tettetattt ttecattete etttecaaag ceatggeeat 120 qcqctcctgt gtacaggtgc ataaacacat cagtgtgcca tccctcacat gcatgtcgtt 180 coccaccct cottoccagg gottotottg gotccagcgt toototggga coctotgcag 240 atacageetg tgetggacce ceagecaggg tgagggetca ttetgetetg tetteceeae 300 tgcctcagtt tcccccaaaa gctgctttca cgtccttcta gtagggggcc tcccatgggg 360 qcaaqqatcc cctttaggat tcaatctttc ctctttgggc agttttggct ttgaqtcccc 420 caqqqatcag ggtgagaatg aagaagagct cagtgagcgg aatgacagca gctgqgtqqq 480 tqqtqtqqqq aqagqctgaq gggaaggcag ctctaagact gggagtggag ttcctggagg 540 tgtggggagg ggggtgtt ttcaatttag aaaaatctca gccagctcga gccgagagag 600 aatgcgaaag aggaagttcg gaaggagcga ggaatggggt gggtggcagc gggggccgct 660 cagttgctgt cgctcttgtc caccagcacg gcgtccgact cctcggtgat ctccagcagc 720 gegtgeaegt eggggetget eeeggeege aggtegeegg eetceeeeg eteegeeeae 780 ctccaccatc tcggtggcct tgagcacttc cacctggccc tcgcggatct tcttgacgtg 840 gaaggtgaag ggtggcacct tgtagaccgc ggtcttggag cgcgcgtaca ccacgtggtc 900 gggcgtgaag gatttgcgca acttgtcccg cgacgtcttc agtttctcgc gccgctcggc 960 gggcaccagg cgcgtgccca gcttgttcat gcgcttctcc agggtgtgcc gcgtcttctc1020 caggittec tiggicita ggcgcgitt ciccaggitc tcgcgggiac gcaccitggi1080 cttctccatc ttctccttgg agaaggcctt cttgaagtcg tccacgcgcc gcaggccctg1140 cgcttgatac gctctgcgcg ggactcctca ataacctcct caacctccac cgcctcgtcc1200 gacgaaaget ccagegeege tgegteetee tegggeeget egecetegee eageteeteg1260 content to togga age of the content to the content ggcagettea etteateetg gtagateatg aetttaaagt tgeggegeeg cageageteg1380 geotegitga cotecagett ettgatetge ecegeetgge geteeagget geogegeaeg1440 gtetteaegt tgaegetgae ettgegeaee tteteeagea gettgeteae egtattgete1500 qtqqtqqcqt qcqccttqcc caqcttqctc agctcqccct ggatqctctq cactqcqccc1560 tocatotocq cotquegete etccagetqt gettqaqtea getqqatetq gtetaeggee1620 ccgatgattt tgtccaggag gctcagcacc agcacgccgt tcacctggtc cgacttgatc1680 agetettetg ageeggeece egaeggetee teegetgeet gageeceage ggaggaaget1740 ccqqqqcctc ggcqatcggg gtacccgggc aagcggccgc

(2) INFORMATION ON SEQ ID NO. 64:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1652 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ctcgagcggc tcgagccgat tcggctcgag cggctcgaga agaagatatg ctagtctgta tttttgctgt gctattgagg atcaggacaa tgaactaatt accctggaaa taattcatcg 120 ttatgtggaa ttacttgaca agtatttcgg cagtgtctgt gaactagata tcatctttaa 180 ttttgagaag gcttatttta ttttggatga gtttcttttg ggaggggaag ttcaggaaac 240 atccaagaaa aatgtcctta aagcaattga gcaggctgat ctactgcagg aggaagctga 300 aaccccacgt agtggttctt gaagaaattg gactgacata actctcctcc cttgttgatg 360 acttettgtg geattteaca cactgtagat ggteactece tteatgteea tgttagetea 420 tggtgtaaga tgatgtcttg tcagtattac tgttttgcta agccgcttca ttcatgccta 480 cacaattttt ttttaaaagg gaactttagt taattaagtg ataagggact taaatatgaa 540 ttagaatggt gcagaaagag ataccttttc tggatatttt aaagtttaaa ggtcagtttc 600 tottaatotg attatgtgca catatgaaaa tggcacatca tatacatgta aaatcaggca 660 gtatacattt attaattact gtatttgaca aaggaaactc ttaaattata atgtgaaacc 720 tggttttatg aaaccaaaga ctagtgcagc atttcagcat atgtaaaaag aaaaaaaaa 780 gggaattgac atgtcacata tcaaatgaat ggaaactttg ttgaaacttt aaaaagcaaa 840 tttactccaa agacttgtat tggaaattac ataccttttt ttttttttt aaaggactac 900 agattatttt taatgactaa attggagtga tacttcttac actaaaaatt atttcttagg 960 cattctgaat ctgggatgag aaacaggatt gtttcacaat agtaagcaca taatttttaa1020 ggccaaggca catttgactc ctgagatgaa ttttttgtgg tcataatcaa atacttagtt1080 gtttttgatg ccccaaaata aagtgagaat ggtaatttgc caggaattct tcataacagt1140 atcttacaaa aaacgtgttg ctctcttcac agtattatgt gtaaagtcat tgtttaaagc1200 acgaatgttc cctctggggt acttgttaaa gctaaattta ttttgcttcc ctccacttag1260 aagtgctgca cactttacag cagcttcctt tctttccatg gcactgccta gttaacagaa1320 gtcttataaa aatttaaaaa gacacatttc ttacaaaaaa gagttgaatg aggtaaaatg1380 gcattagatg gctctatatt ttttaaagct atgtaattgt tcagcgtcac ttttctaagt1440 acttatacat atctaaacat gtcttcatgg tttatatttt cacttatata tgctgggctg1500 gattaagctt tgttgtgatt gtgaccaaca ttcaggccac gtgagcactg tcttatcaca1560 togocaatta gttgtaataa acgttcaacg tacaaaaaaa aaaaagggcg cagcttccct1620 ggggggaatt actggaagcg gggttaagcg ga

- (2) INFORMATION ON SEQ ID NO. 65:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1085 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
getecetgge etecetetea gacagettgg gggtgtetgt catggecace gaccaggact 60
cctactccac cagcagcacg gaggaggagc tggagcagtt cagcagcccc agcgtgaaga 120
agaagecete catgateetg ggeaaggete ggeacegget gagetttgee agttteagea 180
gcatgttcca cgctttcctc tccaacaacc gcaagctgta caagaaggtg gtggagctgg 240
cgcaggacaa gggctcgtac tttggcagcc tggtgcagga ctacaaggtg tacagcctgg 300
agatgatggc gcgccagacc tccagcacgg agatgctgca ggagattcgc accatgatga 360
cccagctcaa gagctacctg ctgcagagca ccgagctcaa ggccctggtg gaccccgccc 420
tgcactccga ggaggagctc gaagcaattg tagagtctgc cttgtacaaa tgtgtcctga 480
agcccctgaa ggaagccatc aactcatgcc tgcatcagat ccacagcaag gatggttcgc 540
tgcagcagct caaggagaac cagttagtga tcctggccac caccaccact gacctaggtg 600
tgaccaccag cgtgccggag gtgcccatga tggagaagat cctgcagaag ttcaccagca 660
tgcacaaggc ctactcacct gagaagaaga tctccatcct gctcaagacc tgcaaactca 720
tctacgactc catggccctc ggcaacccag ggaagcccta tggggcggat gacttcctgc 780
ctgtgctcat gtatgtgctg gcccgcagca acctcacgga gatgcttctc aatgtggagt 840
acatgatgga gctcatggac cccgccctgc agctggggga gggttcctac tatctgacca 900
ccacctacgg ggccctggag cacatcaaga gctacgacaa gatcacggtg acccggcagc 960
tgagtgtgga ggtgcaggac tccatccacc gctgggagcg ccggcgtact ctcaacaagg1020
cccgggcctc ccgctcctcc gtacagccac ttcatctgcg tgtcgtacct ggagcccgag1080
cagca
```

- (2) INFORMATION ON SEQ ID NO. 66:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1393 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

gggcagggga gggagttgac gggctgacac aggaaactcc cctgaaacct gtttctcagc 60 ttcccggccc agctggggca cccactggaa ggagaggcca ggcggaagac cctggctccg 120 tcatggcctc tgccctgagg ccaccccgtg tccccaagcc taagggtgtc ctgccttcac 180 actactatga gagctttcta gagaagaagg ggccctgtga ccgggattac aagaagttct 240 gggcaggcct gcagggtctc accatttatt tctacaatag caatcgggac ttccagcacg 300 tggagaaget caacttggga geatttgaga aacteacaga tgagatteee tggggaaget 360 cacgtgaccc tggcacccac ttcagcctga ttctccggaa tcaggagatc aagttcaagg 420 tagagacctt ggagtgtcgg gaaatgtgga aaggcttcat cttaacggtg gtggagctcc 480 gtgtcccgac cgacttgacc ctgcttcctg ggcacctata catgatgtct gaagtcttgg 540 ccaaagagga ggcgcccgt gcactggaga caccctcgtg cttcctgaag gtgagccggc 600 tggaggcaca actgctcctg gagcgctacc ccgagtgcgg gaacctgctg ctgcggccca 660 gcggggacgg cgccgacggt gtcggtcacc acgcggcaga tgcacaacgg gacgcacgtg 720 gtccggcatt acaaggtgaa gcgggagggg ccccaagtac gtgatcgatg tggaacagcc 780 gttctcttgc acctccctgg acgccgtggt caactatttc gtgtcgcata ccaaaaaggc 840 gctggtgcca ttcctgttag acgaggacta cgagaaggtg ctaggctacg tggaagccga 900 taaggagaat ggcgagaatg tgtgggtggc gccctccgct ccgggcccag gtcctgcacc 960 ctgcacaggt ggccccaagc cgctgtcacc tgcgtctagc caggacaagc tgccccact1020 gcccccacta ccgaaccagg aagagaacta cgtgacccct attggagatg gcccagctgt1080 tgactatgag aaccaagatg tggcttcctc tagttggcca gtcatcctga agccaaaqaa1140 gttgccaaag cctcctgcca agcttccaaa gccacccgtt ggacccaagc cagagcccaa1200 agtetttaat ggtggettgg geagggaage tgeeagttea gttteageee ageetettet1260 ttccccacag gccgggctgg gcagacatgg acggcagagt tacagaagaa gctgggagaa1320 gaggcggggc actggtagca tggtttcgga cacaccaggg accagcgggt tagttccagg1380 gcgggccagg tgg 1393 1.35 Jill 3

(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1248 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:
qqcacqaqqa aqttaaqatc atacatqcqq atqtqctqqt aacctqcaaq aaqcaatcat 60
gctgcggtcc ggtgtgacct cccaaggcat tcaccctggg agtccctggt gctgcacccc 120
aacccaggca gagctcatcg tgggtgacca gagcggggct atccacatct gggacttgaa 180
aacagaccac aacgagcagc tgatccctga gcccgaggtc tccatcacgt ccgcccacat 240
cgatcccgac gccagctaca tggcagctgt caatagcacc ggaaactgct atgtctggaa 300
totgacgggg ggcattggtg acgaggtgac ccagotoato cocaagacta agatocotgc 360
ccacacgcgc tacgccctgc agtgtcgctt cagccccgac tccacgctcc tcgccacctg 420
ctcggctgat cagacgtgca agatctggag gacgtccaac ttctccctga tgacggagct 480
gagcatcaag agcggcaacc ccggggagtc ctcccgcggc tggatgtggg gctgcqcctt 540
ctcgggggac tcccagtaca tcgtcactgc ttcctcggac aacctggccc ggctctggtg 600
tgtggagact ggagagatca agagagagta tggcggccac cagaaggctg ttgtctgcct 660
ggccttcaat gacagtgtgc tgggctagcc tgtgacccct cgggactgcc tggtgcaggt 720
ggtggcagct ggagggaccc atgcagcacc caggtcagag cagaccetee eetgeeggee 780
tgcgccactg gacctgatgg ccccctgtgg cgccttgacc tgctgggcca ggctgccctg 840
ggacteteag ecceeagttg ettateeaga tgtgacagag etegaceeaa geeaggetge 900
acactectgg actgggetag cetgeactge etgggaaagt eggeegaggg eccaaagetg 960
ctgaggggtc tgaggctggt gcccaccccc aagctagtgt gttctctgcc cctccctgcc1020
cgcgtttcag ggcctcggtc catagagaac accaccacca tggccaggtg gaagggttta1080
ttagtccctg ccagcagctg tcctccctgg tgcaggtggc ctggccagcc cactggattg1140
gggacgggcc aggctgggcc aggtcggggg ctcagtctgg gaggtaataa aagcagaccg1200
acacgcagat gttgctcggg aaaaaaaaaa aaaaaaaaa aaaaaaaa
                                                                 1248
```

- (2) INFORMATION ON SEQ ID NO. 68:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1099 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

ctcgtgcaat ttcgggcagg gagtgtcaag cctgttgtct taacattttg tataaaaaag aacaacagaa attatctgtc atttgagaag tggcttgaca atcatttgag ctttgaaagc 120 agtcactgtg gtgtaatatg aatgctgtcc tagtggtcat agtaccaagg gcacgtgtct 180 ccccttggta taactgattt cctttttagt cctctactgc taaataagtt aattttgcat 240 tttgcagaaa gaaacattga ttgctaaatc tttttgctgc tgtgttttgg tgttttcatg 300 tttacttgtt ttatattgat ctgttttaag tatgagaggc ttatagtgcc ctccattgta 360 aatccatagt catctttta agcttattgt gtttaagaaa gtagctatgt gttaaacaga 420 ggtgatggca gcccttccct agcacactgg tggaagagac cccttaagaa cctgacccca 480 gtgaatgaag ctgatgcaca gggagcacca aaggaccttc gttaagtgat aattgtcctg 540geeteteage catgacegtt atgaggaaat atcccccatt egaacttaac agatgeetee 600 tctccaaaga gaattaaaat cgtagcttgt acagatcaag agaatatact gggcagaatg 660 aagtatgttt gtttattttt ctttaaaaat aaaggatttt ggaactctgg agagtaagaa 720 tatagtatag agtttgcctc aacacatgtg agggccaaat aacctgctag ctaggcagta 780 ataaactctg ttacagaaga gaaaaagggc cgggcacagt ggcttattcc tgtaatccca 840 acactgtqqa aggccqaqqc aggagqatca cttqagtcca qqagtttqaa acctacctag 900 gcaacatggt gaaaccttgt ctctaccaaa ataaaaatta gctgggcatg gtggcacgtg 960 cctqtqqtcc caqctacttq qgaqqctqaq qtqqqaqcct qqqaqqtcaa qqctqcaqtq1020 agccatgate atgccactge actecateet gggtgacage aagatettgt etcaaaaaaa1080 aaaaaaaaa aagtcgacc

(2) INFORMATION ON SEQ ID NO. 69:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

tttatggagc ctgtactatg taccagatgc agactgtgct agcggttggg gatacagtga 60 tgacttggtc tgcctctagg tggcagggag ccattttggg ttttcgaaca gaaaagtgac120 ataatgaatg ctgagtctt aggaagatta atccaggagt agtctccagg atgtactgga180 aggagagaag ctgaaaccag ggaggctgct gtgtttgcag ttggctgcc agtgctacct240 ctgcagagac aatcaatgtc ctgaaggtag ctggtatgtc tgtgtgcact gacacgagcc300 ttcctaccaa gccccagggg ctccatgctg gagaatgcac gtagggctag ggtgagcact360 aacttcactt caggagagca aggaacagtg tggctcttcc attttcagt tctgtaagca420 catcaccctt tcctccc cttgagctgt gttctctgac agctgtttgt tggtaaagcc480 agcacgaccct aaagcacgtc ccagccttgt ctcctctgtg ctttcccca ccactgctgc540 tgcacgcctc atttgctggg ccactttagt ggtggaacca ttagaggctg agtgacttaa600 aggagattga gtctgtctcg accccgagag agagtggat ggatggatgc atcgtctcat660 ttagaaagtg ttgcctctga ctctaacaca ctcttctctc tttcttacc gccctccctg720 tgtgcgtccc tggggggcg tgggctaaac cccttccgtc cccctttctc ctc

- (2) INFORMATION ON SEQ ID NO. 70:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

tagctccagt ctcagctgta tcatttcta actgatttt acaataaaaa tgagagtaaa 60 aatcagttac tctttctaga cattaattag cacatttacg ttaagactct aagtagtata120 aaatgtaaat tgctgctacc ctactaagtt actgtcagta aatactgtgt gcagtaaatg180 ttgagtatgg attaattgaa ggatacctct acaattattt cctttagtca aggttgtagc240 taagaattgg gcttctgaca tacattcttt ttaatctttt tcgtattggg ttttatagca300 ctaaacctaa tttctaacat attttacac ctgaaatcta cattctaata taaaggtttt360 tttttataac gttcctaaaa tttcaggccc tcagcaggca gtttttgtcc cagttttctt420 caacag

- (2) INFORMATION ON SEQ ID NO. 71:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1417 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

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gccaacette ectececcaa ecetggggee geeceagggt teetgegeae tgeetgttee
teetgggtgt caetggeage cetgteette etagagggae tggaacetaa tteteetgag 120
gctgagggag ggtggagggt ctcaaggcaa cgctggcccc acgacggagt gccaggagca 180
ctaacagtac ccttagcttg ctttcctcct ccctcctttt tattttcaag ttccttttta 240
tttctccttg cgtaacaacc ttcttccctt ctgcaccact gcccgtaccc ttacccgccc 300
cgccacctcc ttgctacccc actcttgaaa ccacagctgt tggcagggtc cccagctcat 360
gccagcctca tctcctttct tgctagcccc caaagggcct ccaggcaaca tggggggccc 420
agtcagagag ccggcactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480
cgtggcttgt gccatggctc tgctgaccca acaaacagag ctgcagagcc tcaggagaga 540°
ggtgagccgg ctgcagggga caggaggccc ctcccagaat ggggaagggt atccctggca 600
gagtctcccg gagcagagtt ccgatgccct ggaagcctgg gagagtgggg agagatcccg 660
qaaaaqqaga gcagtgctca cccaaaaaca gaagaatgac tccgatgtga cagaggtgat 720
gtggcaacca gctcttaggc gtgggagagg cctacaggcc caaggatatg gtgtccgaat 780
ccaggatgct ggagtttatc tgctgtatag ccaggtcctg tttcaagacg tgactttcac 840
catgggtcag gtggtgtctc gagaaggcca aggaaggcag gagactctat tccgatgtat 900
aagaagtatg ccctcccacc cggaccgggc ctacaacagc tgctatagcg caggtgtctt 960
ccatttacac caaggggata ttctgagtgt cataattccc cgggcaaggg cgaaacttaa1020
cctctctcca catggaacct tcctggggtt tgtgaaactg tgattgtgtt ataaaaagtg1080
gctcccagct tggaagacca gggtgggtac atactggaga cagccaagag ctgagtatat1140
aaaqqaqagg gaatgtgcag gaacagagge gtetteetgg gtttggetee eegtteetca1200
cttttccctt ttcattccca ccccctagac tttgatttta cggatatctt gcttctgttc1260
cccatggagc tccgaattct tgcgtgtgtg tagatgaggg gcgggggacg ggcgccaggc1320
attgttcaga cctggtcggg gcccactgga agcatccaga acagcaccac catctaacgg1380
ccgctcgagg gaagcacccg gcggtttggg cgaagtc
                                                                 1417
```

(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO.
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1705 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

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gattcggcat gaggacagag ccctttttga aaataaattg gcattggagt gttttaccct
ctagctgttt tacttagaat gtaacatatg ctgcctaccc acctcaaaat gtctgtactg 120
caagagggcc ctgggcctct gctttccata ttcacgtttg gccagagttg tagtcccaaa 180
gaagagcatg ggtggcagat ggtagggaat tgaactggcc tgtgcaatgg gcatggagca 240
caaggggtca cagcatgcct cctgccttac cgtggcagta cggagacagt ccagaacatg 300
gtcttcttgc cacggggtgt tgttgtctct ggtggtgctg catgtctgtg gctcaccttt 360
attettgaaa etgaggttta eetggatetg getaetgagg etagagecca eageagaatg 420
gggttgggcc tgtggccccc caaactaggg ggtgtgggtt catcacagtg ttgccttttg 480
tetectaaag atagggatet aettttgaag ggaattgtte eteccaaata aatttgettt 540
accttggtcc tttcttttgt gccagtattc aagtggtata gctctgagca gggtcacatt 600
tggccaaacc tgacactgtc ttgctgcatt ctcctttggc aaacatcagg gtcagaattc 660
aggatagece tteetaggge actggaettt etggeatggg ggetgtgttt geacaagtta 720
ttttcatgtt acctggagag tgtccagagg ctgctctgag gctgaggtgt gttccccctt 780
gcctggttcc agctgtcaga gggataccat cctagggtct gggaatccaa ggccacgaga 840
ctccttggtt tgtggtccga gatcctgtac taaggagggt ctggccagag gaacagacca 900
gettttgeae aatgaagege aagggaaeaa gtggtttgee tggtgteeta eetgteetga 960
acctggtcct gtgggccatt gaaaagttag atctgtgatc tctggggttt ttgtggcttt1020
gttcaatgct tccactctag ggcaggcaga gcagtctata ctctcccaag cctgcttgac1080
ctccaagtag agctgataca gagatctgtg aatattgtga tagaaattct ttggtattcal140
tacatttcag ctgcaagtca gcaatttccc aggtaccatg taagctataa aacagtcatt1200
cttaaagaca gaggatagct gtgactcatg ggatcatgag gtccatggct ggttgcaggt1260
tecettttte etteeteagg ttttgtetet teetgtgttg teeceageaa gggagagaet1320
gtggggtgga ttgggagaac agattaggag tatagcaaat gaacccagaa tggaacagtg1380
gggagctaac tgtgaatgag gagagtacct gctgcaggac ctggaggtca ggtgtgaatg1440
ctgtattggc acagggaata aatatcctgg cgtctggagc cttcacctct ccgtcaagtc1500
cttcctgtga tactgccatg gcacaggatc tgagttgcag ctctgcaccc taaatcacac1560
cctgggcatt gtctgggctg cagggctgcc aggttctgta cttgtgtcca gctgtggccc1620
tggatgccgg aaactgggag gggtttcttg tgcccagaat gtagcctgta acgcttgggc1680
gccttttaaa gcccccctg gggcc
                                                                  1705
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(2) INFORMATION ON SEQ ID NO. 74:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1516 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

gtttattctt agtagttgga actaatgtag tctgactaaa atacacatgg gtgtctgctc 60 tgtgatgttt aaacttatct gttttgtttg gttttcattt caggaagcag aagtgcaagc 120 aaagcagcaa gcatgaacct taagcactgt gctttaagca tcctgaaaaa tgagtctcca 180 ttgcttttat aaaatagcag aattagcttt gcttcaaaag aaataggctt aatgttgaaa 240 taatagatta gttgggtttt cacatgcaaa cattcaaaat gaatacaaaa ttaaaatttg 300 aacattatgg tgattatggt gaggagaatg ggatattaac ataaaattat attaataagt 360 agatatcgta gaaatagtgt tgttacctgc caagccatcc tgtatacacc aatgatttta 420 caaagaaaac accetteeet eettetgeea ttaetatgge aacttaagtg tatetgeage 480 tctacattaa aaaggagaaa gagaaataac ctgtctctca ttcctaagtt gcctcattaa 540 ttttcatgaa caagaatatg tacctttttg atgctatatt actgcgatta aaaagttctt 600 gcaggtaatg tttatgatat gttaaacgtt gtaatttctt atcgtaatta taacattccc 660 attettttgt agatgaaact tetacatatt gaaccacaga ttttetgage ttetaaatgt 720 agcettteat tgcacattte agtgateaga atagatatee ttttacaege acaaaageaa 780 tagattcatt cagtggacaa gttccttgtt taactacaca gctatgatgg aatgatatat 840 ccaagtteet tgeeteagtg aaatatgeat atgtatatea tgaaagtggg atgeeaagta 900 agettaaaat ggeattetet ageaaagaga ttagaetttt aaataaetet tataaaacag 960 gttggcgatc atttcccaag attggtttcc cttgagtttt tgctaaaaca aatcttagta1020 gttttgcccg tttaaaacaa ctcacaatcg taaatgctac tattcctaag atatcttacc1080 tttttatttc agtttagcca tgtattgtat gagtgtatta gtctaagcag tgagaatctt1140 ttctatgcct ctattccagc aaaaagtaga agtatcaaat aaaaagggca acttttaaaa1200 tattaageet gaagaettet aaaaagaeaa gaaacatgge etaaataace aacatagatt1260 tacatagtaa gtttcacact accttattac caaaagcaaa cacctcttac tttaaactac1320 attatcatgt atatctattg tatgctggtc tttacttttt gccaaaatca acatataatg1380 aagagatgcc tttgtttcat gagattcaaa cttgatgcta tgctttaaaa taaactcagt1440 acttttagaa acataaaaaa aaaaaaaaa aggcgacccc ccgagtagtg ggcccgcgcc1500 cggggatttt tccggg

(2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1490 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

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qaataaaqqq ctqqccaqac ccaqtqqcqt cctttcccaq acctttcttq qcacaaaqcc 60
tttgctgcct ggcttggagg ccctgcggcc tacattctct ggaccccact atgtgcctgg 120
caaaqqqcta gtgccttgag gaaactgagg tagctgggtt ggtccccttc caggaattca 180
gagtctggtg gcaggggcat gggaaataga cagatgtaat tctatagcct gggcctggca 240
controller coargence caageattge ettacgente cottgence egttagatgg 300
tttcttccgg ttttgcactc tggctgcccc ttggagtctc ctggggagct gtaatatctc 360
tttggagatt cagattgagc tggtctaggt tgtggcccag gcattgggca ttttggaagc 420
ccccaggtgt tttcagcttg cagccaggcc gagagagagc ccctgagtca gatccccatg 480
gtttaggcac acctageggg aggggtggct cctggacccc accgtggttg gagagetgag 540
catgtgtgtg gctttagtgg ggtctgttag ttatgggggt ctgggcactg gagctgcagg 600
acacttggga tcccaggtca gaaagggcca gatgagcaac taggaaagac ttgggggcca 660
gggcggagtg gggtcacctg acactettgt gaggeceett ctagtgeetg etcacacegg 720
aatttcattc actccaagaa gccatcaggg gtaagatacc ttcctttaaa cgtcactaag 780
aaagaagagg cctgccggtg acacagtaag atgccattga tctaaagatg cgtcttgatt 840
tcagaaaggt ccggaagtgg aaagcaggtt tcagggctgc tgaggtacag ggttctcctg 900
taggccccag ggatggtctc aggggtgctg agtgcgtgcg tggtaaatgg atggagccca 960
ggggcgcctc ctgccagtgt cctccaggca ctcaaaccta gcccttctga agccgacctc1020
acgtgacete acageceete etgaaggege etcactgatg acggtgggtg gaataacage1080
ccccagagat gtccaggttt ggaaccccag gacgtgggaa agtgttacct tgcgtggcaal140
aagggacccg gcgcctgtgc ttcagttcag gatttcgtgg tggggagatg accgtggatg1200
gttgaggtgg gccctgagta atcatggggg cccttataag ggaaggggag tcacgagggt1260
ctgcgcatga agcaaggaag cttctggctg tgaagatggc aagaaggcct ggggccaggc1320
gatgaggtgg cccctggagg agctggaaaa ggcattggat tctgccccag agcctccgtg1380
qaqaaacaaa gccgcactga caagacttca gcctggtgaa aaccattttg gactcctgac1440
ctctagaact gtaagataat aaattggtgt ggttttcaac ctctcaaatg
                                                                 1490
```

(2) INFORMATION ON SEQ ID NO. 76:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2513 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

ctcgagccga	ttcggtttca	gcagaaagtg	atggaaaaag	aaactgaaaa	gcgcatttct	60
gaaatcgaag	, atgctgcatt	cctggcccga	gagaaagcga	aacaagatgc	tgaatattat	120
gctgcacaca	aatatgccac	ctcaaacaag	cacaagttga	ccccggaata	tctggagctc	180
aaaaagtacc	aggccattgc	ttctaacagt	aagatctatt	ttggcagcaa	catccctaac	240
atgttcgtgg	actcctcatg	tgctttgaaa	tattcagata	ttaggactgg	aagagaaagc	300
tcactcccct	ctaaggaggc	tcttgaaccc	tctggagaga	acqtcatcca	aaacaaagag	360
agcacaggtt	gatgcaagag	gtggaaatgt	tctccatatc	aagatgtggc	ccaaggggtt	420
aagtgggaac	aatcattata	cggactcttc	agatttacag	agaacttaca	cttcatctgt	480
tccacctctc	ctgcgatagt	cctgggtgct	ccactgattg	gaggatagag	ccagctgtct	540
gacacacaaa	tggtcttttc	agccacagtc	ttatcaagta	tcctatatgt	attecttect	600
aaactgctac	tcatgaatga	ggaaagtctg	atgctaagat	actgcctgca	ctggaatgtt	660
aaacactaaa	tatataacaa	gctgtgtttt	cctaagctga	gatctgttga	ataatgttta	720
cattcgtccc	ccggggaaat	gtatgctcag	ccaccattca	agagatgact	gagaaggaga	780
tggtaagttc	aagaagactg	attgcacctg	ggacccaggc	cctttctttg	ggatccagtc	840
ccagccttca	tccatgtgat	taagatccag	gccgctgaag	ttccccagga	aatgatcttc	900
cacttgagca	accttttact	tgatacgatt	tgcacctttc	tgttttcctg	cagtcagggt	960
ggtggcctgc	agggacctga	gctttgctac	ccaaccagat	tcctcataga	gattcctaat1	1020
cactagtttc	ttgtattcat	aaactcagag	atacagaggg	cttggtttga	agttggggtg]	080
agatgaaacc	tittgctctga	gccaaagctc	tggggccttg	cattccctgc	attgggttga1	1140
tgactgtcag	catcactgcc	gcagcatgct	tgactaaggt	acctggtttt	agccacagcc1	200
acctccttgt.	. atgttacctt	tcagctctgg	ccaagagtgg	gacagggttt	taaccacaaa1	260
taggagcagc	atgcaattcc	tagtgacttg	ctgcacagta	ttgtatcata	attacaggaa1	320
gtttttattt	ttaaaactgg	atctggggta	tattcatttg	ccccatcacc	tctgtctaaal	.380
ggcccaagtc	ctagggctgc	catggtcaca	agcacactga	tgctccttaa'	gattgtttat1	440
ctggagccca	catagtgtgg	aacaaaaagt	cacctagaaa	gcatccttgg	tcatcattot1	500
ctccttccca	cctggcccag	agatgcttaa	atccaagttg	tttctccage	totcacctcc1	560
cccaggagat	caggattcca	ctgacgtcct	gggcagccag	tgaatttaat	tttccatgag1	620
aaacaacaga	gttaacctgt	ggcattagga	gacctacttc	atgtggaccc	tttttttcct1	680
tcagtttaac	ttttctggag	cagtgtgctg	cgtagttcgg	cctgagtttg	tgcagcttgt1	740
taagacaact	cttgtgtacg	ctatgttgaa	gctcaacaaa	aaagtcatgg	gaccacttct1	.800
agaaatcttt	cagctgtcag	gcctgtcagt	ctcatgacag	tttgttggtt	gtgccaaacal	860
ctttatttgg	gaaaggaaag	cccagatttg	aatgggtctt	tcccctgggc	cttatcctat1	920
agaggcattt	gtaatatgga	gaaaataatt	tttcattttt	gctcatttaa	ttctataaat1	980
tctcttata	aatgaatttt	gtgttcttta	gttctcctta	aaagaacttt	tgaattataa2	040
aaataaaatc	tttacctgtc	gaattgttgc	tgcagatgat	tgttgtggaa	aatctggatc2	100
attgacctct	gtgctttcat	tcctagagat	gttttatagt	tacatgagca	aaagctgttg2	160
ccccaaagtg	atggccctgg	aggcggggct	gaggaacagg	gaaatgccgc	tgtgaagtct2	220
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claaatttat	acgttgaaat	gctacctttt	ttaaaataag	aaactaaata	aaattatttt2	400
actatcaaaa	aaaaagaaag	gggagggaag	ggggcggagg	gggtaggagg	ggggggggg2	460
gayggggggg	aggggaatgt	ctcgagaggg	ggggggtggg	ggcgccgtcg	agc 2	513

(2) INFORMATION ON SEQ ID NO. 77:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1962 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRÁND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
- ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

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accgacggcc gccccttttc gtcttttttt tttttacatt tcaaatatat tttattactt 60
tccatcttag aaagaatatg aaacctgcat gcaatgctaa tggtttctga catgtacata 120
gcatataaca cagcagtaca atgcggcata tactgggggg cagtgtgtgg agggggggtt 180
cttaagggta tatgtacaga ggaaagggcg catggtcatc ttagctttcg aaagaggact 240
gcactgttta acattgaaga attacatggg gaatcacaaa tatattgctt tagtactgca 300
tgttctgttg tggtgaggga aagaaacatg ctttgaaggt tttcccttgt caacagaatg 360
tgtgtctgta gctgtgtatt gcgcatgtat tcatatattt ttaagttttc tcctaaggtt 420
tttgctgaca gtgttgggaa cctcacatgc ttctgaagca ttaaatattg aacctgtgaa 480
cctttcagaa atcctcaggt tgggaaagac cccacacctt ctttaaggat catttgtctc 540
gccatcacag gatcttggaa atgtttccta gggtgtgtaa aaattaacca ggggggaatg 600
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aaqcccagga gagcccgtgg cagctgtgcc gaggcgccag gacctctaag cggaaqcttc 780
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cgggcgctta taaagctcag atgtatagtg acgtatggac aaatacaaaa aaaaaaaaa 900
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- (2) INFORMATION ON SEQ ID NO. 78:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 788 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

- (2) INFORMATION ON SEQ ID NO. 79:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

- (2) INFORMATION ON SEQ ID NO. 80:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2263 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

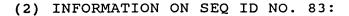
attacgacaa	ctcttctaca	tgtaagaaag	gaaaggtatt	ccctgggaag	atttcagtga	60
cagtatcaga	aacatttgac	ccagaagaga	aacattccat	ggcctatcaa	gacttgcata	
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gtggtgggc	ccctgagtgt	gcgtgcgtgc	ccggctacca	ggaagatgct	aatgggaact	600
gccaaaagtg	tgcatttggc	tacagtggac	tcgactgtaa	ggacaaattt	cagctgatcc	660
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- (2) INFORMATION ON SEQ ID NO. 81:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1284 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

aaaaatgggc taaactagct ccagagaact tgtgaattct ttgctaaagc ctctggcaaa aacggcattt gatgaagcaa ttgctgaatt ggatacgctg aatgaagagt cttataaaga 120 cagcactctg atcatgcagt tacttaggga caatctcact ctgtggacat cggaaaacca 180 gggagacgaa ggagacgctg gggagggaga gaactaatgt ttctcgtgct ttgtgatctg 240 ttcagtgtca ctctgtaccc tcaacatata tcccttgtgc gataaaaaaa aaaaaaaaa 300 aaaaaagagt cgtacgtcga ctttcgattt ttcacagcct cagcctagga aaaatggttc 360 atgggataaa cagctggtat ttgtatctaa aactcagatt ggtcacataa atgccacggc 420 attccgaagt tttgattttg attaacattg acaggattac tgtgtgttta attttttaaa 480 aactgaacac tgtgattatg gggttttgta atttagcaga actcttactg gtagaaaaaa 540 tagacctgaa ttatgtgtaa ctttttggaa ggtttaatct gatatcaaaa taatcattga 600 aatacaattc cattgtaaag ttgtacagaa agttatagag attatattgt gatgctggaa 660 cttggagtga gacacacatc atttggcatt tgagttgaat ggtaattcac agtaatgctg 720 ccgttgttcg ggacttaaag acacttgacc tgtttgggct gttgccactt aaaagttcat 780 gaccacaaat gtccacagtg tetteetetg aggaaacteg aateetgaaa tggaaattet 840 ttgtggcaga taactggctt atgacacctt gaaaagttca agtgctcata taacacacca 900 cactgaaccc cctttcctac agcaatatgt tcactatgtt accaatttgc aacttgtgct 960 tcaatagtgg aatctacttt cattgttaac actgagctaa agaaaaaaag ccgtgtgttt1020 tatgaatgac cttatctgtt tcctggataa tacctttaag aataatgtcc tgagtcaggc1080 gtggtggtgc gtgcatctag tcccaactat ttgggaggct gaggcaggag gatcgcttgal140 gcccaggagt ttaaagctgc agtgccctgt ggttgcacct gtgaataact gcactccagc1200 ctgggcaaca tagcgagacc tcatctccaa aaaagaaaaa aacacaaaag gatgtgtctg1260 taagaggctt ccctggggga ccag

- (2) INFORMATION ON SEQ ID NO. 82:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1335 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

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gggtgacata atgacaggtt aaatatttgt gattcattga ttaaatatta tttaaagaaa 60
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accaagcage aaactgcagt agtttgtgaa ggattctaat atggggttca ggaatageet 180
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tgagggttgg tcttgctgat ccttcagtta gctctaaatt ctggcaactc cttgtaattc1260
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ccccgtcttc ccagg
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(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

ggcttgtggc ggctctgcca caggggcagg tgttgagggg ctcccggtcc ggctgccgcc 60 geteccege teeggaceeg gggeteccee tagegeeget gaggageege etetgeggte 120 caggagggcg caggagcggg actgagagcg cctggaggct cgagcagagg atagaaggac 180 aaqqacaqaa tcaccagcac tggctgaagg taccttaaca tggggaatct tcttaaagtt 240 ttgacatgca cagacettga geaggggeea aatttttee ttgattttga aaatgeeeag 300 cctacagagt ctgagaagga aatttataat caggtgaatg tagtattaaa agatgcagaa 360 ggcatcttgg aggacttgca gtcatacaga ggagctggcc acgaaatacg agaggcaatc 420 cagcatccag cagatgagaa gttgcaagag aaggcatggg gtgcagttgt tccactagta 480 ggcaaattaa agaaatttta cgaattttct cagaggttag aagcagcatt aagaggtctt 540 ctgggagcct taacaagtac cccatattct cccacccagc atctagagcg agagcaggct 600 cttgctaaac agtttgcaga aattcttcat ttcacactcc ggtttgatga actcaagatg 660 acaaatcctg ccatacagaa tgatttcagc tattatagaa gaacattgag tcgtatgagg 720 attaacaatg taccggcaga aggagaaaat gaagtaaata atgaattggc aaatcgaatg 780 tctttgtttt atgctgaggc aactccaatg ctgaaaacct tgagtgatgc cacaacaaaa 840 tttgtatcag agaataaaaa tttaccaata gaaaatacca cagattgttt aagcacaatg 900 gctagtgtat gcagagtcat gctggaaaca ccggaataca gaagcagatt tacaaatgaa 960 qaqacaqtqt cattctgctt gagggtaatg gtgggtgtca taatactcta tgaccacgta1020 catccagtgg gagcatttgc taaaacttcc aaaattgata tgaaaggttg tatcaaagtt1080 cttaaqqacc aacctcctaa tagtgtggaa ggtcttctaa atgctctcag gtacacaaca1140 aaacatttga atgatgagac tacctccaag caaattaaat ccatgctgca ataacaattc1200 tggaataagc acctgctgta gacagaagac agtattctgc aatgactgag aatgcagttt1260 tttagtgatt gcaattacta tctcatttat tcttgctttt atttctttcc tctgttcctc1320 ttccctcttt tttaatcatg ttcttaagac ttcttttctg tgccaaaatc agtaaagtta1380 cactetquaq qqatateate ettteaaacg ggccatetaa ggcagetaat tatgcattge1440 attggggtct ctactgagaa aaattctgtg acttgaacta aatattttta aatgtggatt1500 ttttttgaaa ctaatattta atattgcttc tcctgcatgg caaaactgcc tattctgcta1560 tttaaaaacc ctcaatgact ttattttcta ctgccgcctt tttcatgtgc aaccaaaatg1620 aaaatgttta aattaactgt gttgtacaaa tggtacccaa cacaaacttt ttttaaatta1680 gtaatacttt tgtttaaagt tttaagtttg cattttgact ttttttgtaa ggatgtatgt1740 tgtgtgttta acctttatta actaacgtta aaagctgtga tgtgtgcgta gaatattacg1800 tatgcatgtt catgtctaaa gaatggctgt tgatgataaa ataaaaatca gctttcattt1860 ttctaaaaaa aaaaaaaaaa aaaaaaaaaa 1890

- (2) INFORMÁTION ON SEQ ID NO. 84:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1829 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

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tcagggcagg gtggcagttt cccttgagca aagcagccag acgttgaact gtgtttcctt1020
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aaggcacgtt ttagagtctc ttgtcttaat gattatgtcc atccgtctgt ccgtccattt1680
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caaccatgaa gcaaaaatcc gttacatgtg ggtctgaact tgtagactcg gtcacagtat1800
caaataaaat ctataacaga aaaaaaaaa
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(2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2358 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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gcgccgcccg	ctcggctccc	atagegeeeg	cgacagggtc	cggacgccgc	ccgaacatgg	120
actccgccgg	ccaagatatc	aacctgaatt	ctcctaacaa	aggtctgctg	tctgactcca	180
		acaggtgtgg				
		ctcagggctg				300
		gccaaggaga				360
		ctgaaacaga				420
-		acttctgaga				480
		actcaggaaa				540
		tctgccatca				600
		gaccgagttg				660
		ctcccttcct				720
		tgtggttgct				780
		tctgttcagc				840
		gcccatccac				900
		acacagatgt				960
		gggtgcagga				.020
ttgagccaaa	gcccaggctc	cctttgggaa	tcatgttagc	ccatcagaat	gttgaaggat1	.080
		ataagtggca				
		atcacccagc				
		ctgtccattt				
		cgcgaatcta				
		aaagtttaaa				
attatttctt	tggactcaag	ctgaaataca	agccttacat	tgccttatgc	tttatttctt1	440
		agatgagggt				
tttacacctg	gcctgcgtgg	cagcctcttc	cagttgaggt	gttttatgtc	acgcacactc1	L560
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		tgagcctctg				
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		cctgcatgtc				
		gacactgagg				
tcccgggagg	ggaagggctg	ctcagctcaa	ggtgtcctgt	tcggtagagc	aagtgtcctc2	2100
tgacagccgt	gtccccggac	agttcagaca	cccttgggga	tggcactcca	cacacgacaga	2160
agatgcaggg	gccagggaag	cccagcgctc	ggtgcccttc	gtccagggtt	aaaatcggcc	2220
		caggttgtgc				
		tttgtcaata				
aaaaaaaaa						2358
•		·			-	

- (2) INFORMATION ON SEQ ID NO. 86:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1646 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

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gaggtccgcc ctccccttca gcgacttggt ctgtgttttg gcagttgccg cgacaacagt 180
cacttccggg aagggggtct gcgaatctcc ttccgtcggt ccgctcagaa tcaqctqtcc 240
tetcagactg tgtgggtggt ttecceggee geageteegt aegggettgg attgetggge 300
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 tagccgaaca tggcatattt ctccctccta atatgcaagg actgaccgat gatcagattg 780
 aagaattgaa attgaaggat gaatggggtg aaaaatgcgt acccagcgga ggtgcagtgt 840
ttaaaaagga tgatattgga cgaaggaatg ggcaagctcc aaatgagaag atgaagcaag 900
tgttaaagaa gactatagaa gaagccaaag caataatatc taagaaacaa gtggaagccg 960
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(2) INFORMATION ON SEQ ID NO. 87:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3096 base pairs
 - (B) TYPE: Nucleic acid. (C) STRAND: individual

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

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egeegeeace	atgaacaaga	agaagaaacc	gttcctaggg	atqcccqcqc	ccctcggcra 180
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agaacacctt	ctgattgage	aattaccata	accartetas	garggaga	ggccgcatca2940
atgtggaagg	actctgaget	atatectect	tcattanane	yrgggcagg	gttgggccgc3000
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(2) INFORMATION ON SEQ ID NO. 88:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1906 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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tecetytyaa tyatyyaaaa eeteacatey teeaetteea ytatyayyte aceyayytya 420
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- (2) INFORMATION ON SEQ ID NO. 90:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

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- (2) INFORMATION ON SEQ ID NO. 91:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2142 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN .
 - (C) ORGAN:

(vii) OTHER ORIGIN: (A) LIBRARY: cDNA library

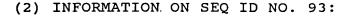
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

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acggctcatt	ctgctcccc	gggtcggagc	ccccggagc	tgcgcgcggg	cttgcagcgc 180
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			ccgacttctc.		agaattgcaa 480
			cggcatcgaa		
caacctgctg	ggccacgaga	ccatgaagga	ggtgctggag	caggccggcg	cttggatccc 600
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					acccattgta1980
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(2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1111 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

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ggttccactt tgccggtgga agggggcttc tgggcctgct gagctccctc cacacacctc1020
aagccccatg ccgtgctcat cctaccccca atccctccaa taaacctgat tctgctgccc1080
aaaaaaaaa aaaaaaaaaa aaaaaaaaag g
                                                                 1111
```



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

atttaaagcc tggattgtaa ccagattttc tttttcccc cttctcagct gtagatatga 60 tatctccttt cagggcccca gcttaagggc aaagtgagtt aatgtgtaga caaaggcgag120 ggacaagaga gagttaacat ctagacagtg gaaaaagcca tggtgtgtgg tttctgggaa180 ccaccaacac ttgcaggttt agcttttcc cagggttgac tacaagaaag aaaaccatgt240 ttttgcaaga ttaaaatgtg gttgagtgtg cctaaattaa ccatccccat ttttatcata300 tttccaccat cacttcaggg ttttaagagt cagtgctcac ctgggcggac tggtagtaca360 ttttgcttct tagaaagcta agtcctggt tccgtctgat ttttaggttcc aggaacttcc420 tgagaacacc cgatcgcaga gggtaatttt ctggagtttg ttttgcaggg atagctggga480 gtatggccac cctgctccac gatgcggtaa tgaatccagc agaagtggtg aagcagcgct540 tgcagagtgt caactcgcag ggggccttc taccggagct gagccctatc tcgtgcc 657

- (2) INFORMATION ON SEQ ID NO. 94:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 863 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

gcggtcggta gtgcggcgt gtttaaagat ggcggcggag gaacctcagc agcagaagca 60 ggagccgctg ggcagcgact ccgaaggtgt taactgtctg gcctatgatg aagccatcat120 ggctcagcag gaccgaattc agcaagagat tgctgtgcag aaccctctgg tgtcagagcg180 gctggagctc tcggtcctat acaaggagta tgctgaagat gacaacatct atcaacagaa240 gatcaaggac ctccacaaaa agtactcgta catccgcaag accaggcctg acggcaactg300 ttctatctgg gctttcggat tctcccactt ggaggcactg ctggatgaca gcaaggagtt360 gcagcggttc aaggctgtgt tccacaagaa gtcaggagaccc ctggtgtccc agggcttcac420 tgaattcaca attgaggatt tccacaacac gtcaatgac ctgattgagc aggtggagaa480 gcaggacctc gtcgggcgc tcacctcggg ctacctgcac cagagcacct ccgactacct540 tgtggtctac gagggtggac ggactgtcaa ggagttctgc cagcaggagc agccactcactcatc gagggttgac ggactgtcaa ggagttctgc cagcaggagc tggagcccat660 gtgcaaggag agcgaccaca tccacatcat tgcgctgcc caggccctca gcgtgtccat720 ccaggtggag gaccacac gcggcaggg cggcaccacc aatccgcaca tcctcctga780 ggccttccga gcccaaggtc ttaaccttgtt ttaaccaca tggggcaatt taggtattgc840 tttttacaaa taggggtttg gtt

- (2) INFORMATION ON SEQ ID NO. 95:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1015 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

aattoggaac gagggogoot gcaagcoatg atgaccoaco tgcatgtgaa gtotacagaa 60 cccaaagctg cccctcagcc cctgaatctg gtatcaagtg tcaccctctc caagtccgca 120 teggaggett etecacagag ettaceteat actecaacga ecceaacege ecceetgact 180 cocgtcaccc aaggcccctc tgtcatcaca accaccagca tgcacacggt gggacccatc 240 cgcaggcggt actcagacaa atacaacgtg cccatttcgt cagcagatat tgcgcagaac 300 caagaatttt ataagaacgc agaagttaga ccaccattta catatgcatc tttaattagg 360 caggocatto togaatotoo agaaaagoag otaacactaa atgagatota taactggtto 420 acacgaatgt ttgcttactt ccgacgcaac gcggccacgt ggaagaatgc agtgcgtcat 480 aatcttagtc ttcacaagtg ttttgtgcga gtagaaaacg ttaaaggggc agtatggaca 540 gtggatgaag tagaatteea aaaacgaagg ceacaaaaga teagtggtaa eeetteeett 600 attaaaaaca tgcagagcag ccacgcctac tgcacacctc tcaatgcagc tttacaggct 660 tcaatggctg agaatagtat acctctatac actaccgctt ccatgggaaa tcccactctg 720 ggcaacttag ccagcgcaat acgggaagag ctgaacgggg caatggagca taccaacagc 780 aacgagagtg acagcagtcc aggcagatct cctatgcaag ccgtgcatcc tgtacacgtc 840 aaagaagagc ccctcgatcc agaggaagct gaagggcccc tgtccttagt gacaacagcc 900 aaccacagtc cagattttga ccatgacaga gattacgaag atgaaccagt aaacgaggac 960 atggagtgac tatcggggcg ggccaacccc gagaatgaag attggaaaaa aaaaa

- (2) INFORMATION ON SEQ ID NO. 96:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2532 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

gctcgatgtg	caagtgaagg	atgattccag	ggccctgact	ttaggagcac	tgacgctgcc	60
tctggcccgc	ctgctgactg	ccccagaact	catcctggac	cagtggttcc	agctcagcag	120
ctctggtcca	aactccagac	tctatatgaa	actagtcatg	aggatcctgt	acttggattc	180
atcagaaata	tgcttcccca	cggtgcctgg	ttgtcctggt	gcttgggacg	tggacagtga	240
gaatccccag	agaggcagca	gtgtggatgc	cccacctcga	ccctgtcaca	cgactcctga	300
tagccagttt	gggactgagc	atgtgcttcg	gatccatgta	ttagaggccc	aggacctgat	360
tgccaaagac	cgtttcttgg	ggggactggt	gaagggcaag	tcagacccct	atgtcaaact	420
aaagttggca	ggacgaagct	tccggagcca	tgttgttcgg	gaagatctca	atccccacta	480
gaatgaggtt	tttgaggtga	tcgtcacatc	agttccaggc	caagagctag	aggttgaagt	540
ctttgacaag	gacttggaca	aggatgattt	tctgggcagg	tgtaaagtgc	gtctcaccac	600
agtottaaac	agtggcttcc	ttgatgagtg	gctgaccctg	gaggatgtcc	catctggccg	660
cctgcacttg	cgcctggagc	gtctcacccc	ccgtcccact	gctgctgagt	tagaggaggt	720
gctgcaggtg	aatagtttga	tccagactca	gaagagtgcg	gagctggctg	caaccctact	780
atccatctat	atggagcggg	cagaggacct	cccgctgcga	aaaggcacca	agcacctcag	840
cccttatgct	actctcactg	tgggagatag	ttctcataaa	accaagacta	tttcgcaaac	900
ttcagcccct	gtctgggatg	agagtgcctc	ctttctcatc	aggaaaccac	acactgagag	960
cctagagttg	caggttcggg	gtgagggcac	tggcgtgctg	ggctcattat	ccctqcccct1	.020
ctcagagctc	ctcgtggctg	accagctctg	cttggaccgc	tggtttacac	tcagcagtggl	.080
tcaggggcag	gtgctactga	gagcacagct	agggatcctg	gtgtcccagc	actcgggagt1	140
ggaagctcat	agccacagct	acagccacag	ctcctcatcg	ctgagtgaag	aaccagagct1	200
ctcgggggga	ccccctcaca	tcacctcctc	agccccagag	ctccggcagc	qcctaacaca1	260
tgttgacagt	ccccttgagg	ctccagccgg	gcctctgggc	caggtgaaac	tgactctgtg1	320
gtactacagt	gaagaacgaa	agctggtcag	cattgttcat	ggttgccggt	cccttcgaca1	380
gaatggacgt	gatcctcctg	atccctatgt	gtcactgttg	ctactgccag	acaagaaccg1	440
aggcaccaag	aggaggacct	cacagaagaa	gaggaccctg	agtcctgaat	ttaatgaacg1	500
gtttgagtgg	gaactccccc	tggatgaggc	ccagagacga	aagctggatg	tctctqtcaal	560
gtctaattcc	tccttcatgt	caagagagcg	tgactgctgg	ggaaggtgca	gctggaccta1	620
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aagggcagct	cctaggagct	ggcgagtccc	agcctgactg	ctctgtcttc	ctaccttcat1	740
ctcgctccat	caccgcctca	atgtgatgag	cctaaagcta	gggtccaagg	gcagagcctgl	800
tgcccttcag	ccctttcacc	taacaggccc	atattcgggc	ctttqcctqa	ccaaagagaa1	860
gaaccgtatg	ttccctttac	tgcacggcct	ttatccttct	gggcccctag	ggcggggacc1	920
tgagctggct	gtttcctgct	ttgcctgcac	attgttctcc	cttcctccca	actcctcagg1	980
gccttctgta	tctgtgcctg	gccagtggca	gcactagcag	tggtattagc	ttatqccaaa2	040
tacagetttg	gaaggatctt	tttttcttta	actagatggt	caccttcttc	cctaccacac2	100
atgggtggga	aggtggacag	gctaacctct	ccagctgtga	gcctcttaga	ctactgcatg2	160
tagcaaatgt	tcagcagctc	aggcccccat	gtccagttct	gtccccactg	tcctcaaccc2	220
tgtcctgaaa	attctactgc	tttgatggct	ggggccagtc	tcttgtcact	ttggaaactg2	280
aggacgcgtg	gattctactc	aagcctccaa	gtagtggcat	atcagtcttg	gagctcctag2	340
ctggtgatac	ggagagggct	ttggaggact,	tgggacagca	gggccaattt	ttttgcccaa2	400
gtgcctaggc	tgctaactca	ctgactagaa	cttaatctgg	tactttacag	ttttgcacca2	460
actctgccaa	gccactggat	cttacattaa	acatcatact	caaaaaaaa	aaaaataaaa2	520
ataaaaaaa	aa					532
	-					

- (2) INFORMATION ON SEQ ID NO. 98:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 776 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO.
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

- (2) INFORMATION ON SEQ ID NO. 99:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 629 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

cggctcgact tccgttactt gctgcggagg accgtgggca gccagggtcg gtgaaggatc 60 ccaaaatggc tgggcgaaaa cttgctctaa aaaccattga ctgggtagct tttgcagaga120 tcataccca gaaccaaaag gccattgcta gttccctgaa atcctggaat gagaccctca180 cctccaggtt ggctgcttta cctgagaatc caccagctat cgactgggct tactacaaagg240 ccaatgtggc caaggctggc ttgggtggatg actttgagaa gaagtttaat gcgctgaagg300 ttcccgtgcc agaggataaa tatactgccc aggtggatgc cgaagaaaaa gaagatgtga360 aatcttgtgc tgagtgggtg tctctctaa aggccaggat tgtagaatat gagaaagaga420 tggagaagat gaagaactta atccatttg atcagatgac cattgaggac ttgaatgaag480 cttcccaga aaccaaatta gacaagaaaa agtatcccta ttggcctcac caaccaattg540 agaatttata aaattgagtc caggaggaag ctctggccct tgtattacac attctggaca600 ttaaaaaataa taattaca aaaaaaaa

- (2) INFORMATION ON SEQ ID NO. 100:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 757 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

gcggggagc agggggacac cagggtgaat caggaagacc cgaggggtgg cccccaccct 60 ttctccaccc acgcggcagg ttccaggtgc cctggctgga gtcagtcctc atcgtagtcal20 gcaacaacat tgacgaggag gcgctggccc gactggccca ggagggcagt gaggtgaatg180 tcattggcat tggcaccagt gtggtcacct gccccaaca gccttccctg ggtggcgtct240 ataagctggt ggccgtgggg ggccagccac gaatgaagct gaccgaggac cccgagaagc300 agacgttgcc tgggagcaag gctgctttcc ggctcctggg ctctgacggg tctccactca360 tggacatgct gcagttagca gaagagccag tgccacaggc tgggcaggag ctgagggtgt420 ggcctccagg ggcccaggag ccctgcaccg tgaggccagc ccaggtggag ccactactgc480 ggctctgcct ccagcagga cagctgtgt agccgctcc atccctgga gagtctagag540 ccttggcca gctgtccctg agccgactca gccctgagac cagggggct cggagccctg600 cacagtacca ggtggtgctg tccgagaggc tgcaggccct ggtgaacagt ctgtgtgcgg660 agcagtccc ctgagactcg gagcgggcg gactggaaca aacacgaatc actcactttt720 ccccacagga agaggaggtg aggggagg

- (2) INFORMATION ON SEQ ID NO. 101:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1262 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

aatttgttga agagtgattc tccctcatcc tctgcaaaca ttccataggc gataggaaga actatgeete tgecaagett tetgagttge tgecagaaga agttgaagea gaagtgaaag 120 cagctgcaga gatatcaatg ggaacagagg tttcagaaga agatatttgc aatattctgc 180 atctttgcac ccaggtgatt gaaatctctg aatatcgaac ccagctctat gaatatctac 240 aaaatcgaat gatggccatt gcacccaatg ttacagtcat ggttggggaa ttagttggag 300 cacqqcttat tgctcatgca ggttctcttt taaatttggc caagcatgca gcttctaccg 360 ttcaqattct tggagctgaa aaggcacttt tcagagccct caaatctaga cgggataccc 420 ctaaqtatqq tctcatttat catgcttcac tcgtgggcca gacaagtccc aaacacaaag 480 gaaagatttc tcgaatgctg gcagccaaaa ccgttttggc tatccgttat gatgcttttg 540 qtqaqqattc aaqttctgca atgggagttg agaacagagc caaattagag gccaggttga 600 gaactttgga agacagaggg ataagaaaaa taagtggaac aggaaaagca ttagcaaaaa 660 cagaaaaata tgaacacaaa agtgaagtga agacttacga tccttctggt gactccacac 720 ttccaacctg ttctaaaaaa cgcaaaatag aacaggtaga taaagaggat gaaattactg 780 aaaagaaagc caaaaaagcc aagattaaag ttaaagttga agaagaggaa gaagaaaaag 840 tggcagaaga agaagaaaca tctgtgaaga agaagaagaa aaggggtaaa aagaaacaca 900 ttaaggaaga accactttct gaggaagaac catgtaccag cacagcaatt gctagtccag 960 agaaaaagaa gaaaaagaaa aaaaagagag agaacgagga ttaacagaaa ggaattacga1020 ttatatcacc cggacacaca tcatgcttaa gattcaactg ggagcatacc agggatgctc1080 tctaacgtaa tcaagggaag gttcagtaag acaaagtgat ttatcatcta taacttcaaal140 cctatttgtc ttgacatcaa ctctgttaac cttatgtcat catttcttag agtctttgat1200 1262

(2) INFORMATION ON SEQ ID NO. 102:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1281 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

qqcqqaaqta qccqcaqqca tqqcqqcqqc tatqccqctq ttqctctqct cqtcctqttq ctcctggggc ccggcggctg gtgccttgca gaacccccac gcgacagcct gcgggaggaa 120 cttgtcatca ccccgctgcc ttccggggac gtagccgcca cattccagtt ccgcacgcgc 180 tgggattcgg agcttcagcg ggaaggagtg tcccattaca ggctctttcc caaagccctg 240 gggcagctga tctccaagta ttctctacgg gagctgcacc tgtcattcac acaaggcttt 300 tggaggaccc gatactgggg gccacccttc ctgcaggccc catcaggtgc agagctgtgg 360 gtctggttcc aagacactgt cactgatgtg gataaatctt ggaaggagct cagtaatgtc 420 ctctcaggga tcttctgcgc ctctctcaac ttcatcgact ccaccaacac agtcactccc 480 actgeetect teaaacceet gggtetggee aatgacactg accaetactt tetgegetat 540 getgtgetge egegggaggt ggtetgeace gaaaacetea eeceetggaa gaagetettg 600 ccctgtagtt ccaaggcagg cctctctgtg ctgctgaagg cagatcgctt gttccacacc 660 agctaccact cccaggcagt gcatatccgc cctgtttgca gaaatgcacg ctgtactagc 720 atctcctggg agctgaggca gaccctgtca gttgtatttg atgccttcat cacggggcag 780 ggaaagaaag actggtccct cttccggatg ttctcccgaa ccctcacgga gccctgcccc 840 ctggcttcag agagccgagt ctatgtggac atcaccacct acaaccagga caacgagaca 900 ttagaggtgc acccacccc gaccactaca tatcaggacg tcatcctagg cactcggaag 960 acctatgcca totatgactt gottgacacc gocatgatca acaactotcg aaacctcaac1020 atccagetea agtggaagag acceeeagag aatgaggeee eeceagtgee etteetgeat1080 gcccagcggt acgtgagtgg ctatgggctg cagaaggggg agctgagcac actgctgtac1140 aacacccacc cataccgggc cttcccggtg ctgctgctgg acaccgtacc ctggtatctg1200 eggetgttae atecaetaee ageetgeeca ggaceggetg caaceceaee teetggagat1260 gctgattcag ctgccggcca a

- (2) INFORMATION ON SEQ ID NO. 103:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 716 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

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gggccccaga aagagaccaa tgtgttgtgc gacgggtggg tggcagtggc agtggcagat 60 ggtaccaggc gccccagaac tctaaggggc ctcaagtagt ttaaaacctc ggaggctgcc120 tgacttgggg ccaagggtt ctatgctcag gcctgacccc tcatggatta gtttctgctg180 gaaaaacttt ttctgccctc ggccaggtct ctatctcctt ctgccttaac atattttgga240 aggttggttc ccagcagaga cggggccatg ggctcacact ctgacctctc ccacggcatt300 agccctgtct cagcctctgg gctgttacgc aagttaattc ctgcacaaga ctcacaacag360 ggctgtggag gaagcaaagg agcccttttt atgcctctgt agtaggactg agaggggccc420 tctggccagc gtgagcctgc tggttcttcc cggactgtac caggccttga ggcgggggtat480 ggaaacgccc cactctgggg cctggcttgg ggaagggag gcggcagggg ttctttgggc540 ttctcgaggg tataatctga gctctctgg gaacgtgtgt ccatttgtag gcagtagtcc600 gacacgtcgg gggactcaac tttacactgg gacaatctgt gtgtggtctg ttttgtagaa660 attcatcac acaagagagt ggaggcatga acaggggtgg ccttcctcgg atctc
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(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1160 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

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tttgttgttg gagaaaggag agaaaggaaa gcgcgagggg ccgccgccac caccagcgca
gagteetgga getgtgagga gattegggee gteaceetge eteceetgeg tecegeeace 120
ggccgcttct gtcctcggac ccattccaac aatctcgtaa aacatggtgg attactatga 180
agttctaggc gtgcagagac atgcctcacc cgaggatatt aaaaaggcat atcggaaact 240
ggcactgaag tggcatccag ataaaaatcc tgagaataaa gaagaagcag agagaaaatt 300
caagcaagta geggaggeat atgaagtget gteggatget aagaaaeggg acatetatga 360
caaatatggc aaagaaggat taaatggtgg aggaggaggt ggaagtcatt ttgacagtcc 420
atttgaattt ggcttcacat tccgtaaccc agatgatgtc ttcagggaat tttttggtgg 480
aagggaccca ttttcatttg acttctttga agaccctttt gaggacttct ttgggaatcg 540
aaggggtccc cgaggaagca gaagccgagg gacggggtcg tttttctctg cgttcagtgg 600
attrccgtct trtggaagtg gattrcttc trttgataca ggattractt carrigggtc 660
actaggicae gggggeetea etteattete tiecaegtea titiggtggta gtggeatggg 720
caacttcaaa tcgatatcaa cttcaactaa aatggttaat ggcagaaaaa tcactacaaa 780
gagaattgtc gagaacggtc aagaaagagt agaagttgaa gaagatggcc agttaaagtc 840
cttaacaata aatggtgtgg ccgacgacga tgccctcgct gaggagcgca tgcggagagg 900
ccagaacgee etgecageee ageetgeegg ceteegeeeg cegaageege eeeggeetge 960
ctegetgetg agacaegege eteactgtet etetgaggag gagggegage aggaeegaee1020
tggggcaccc gggccctggg accccctcgg cgtccgcagc aggattgaaa gaaggtggcal080
agaggaagaa gcagaagcag agagaggagt ttgaaggagg aaggaagttg gaccaaaggc1140
attgattaga ccggattttt
```

- (2) INFORMATION ON SEQ ID NO. 105:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1040 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
agcatccgct tccggttccc agactgaatt gtcagtgagc ggagtctgag gtcgctgtgg 60
actgcccact gggccttgcc cgagatggac agccggattc cttatgatga ctacccggtg 120
gttttcttgc ctgcctatga gaatcctcca gcatggattc ctcctcatga gagggtacac 180
cacceggact acaacaatga gttgacceag tttctgcccc gaaccatcac actgaagaag 240
cctcctggag ctcagttggg atttaacatc cgaggaggaa aggcctccca gctaggcatc 300
ttcatctcca aggtgattcc tgactctgat gcacatagag caggactgca ggaaggggac 360
caagttctag ctgtgaatga tgtggatttc caagatattg agcacagcaa gqctqttqaq 420
atcctgaaga cagctcgtga aatcagcatg cgtgtgcgct tctttcccta caattatcat 480
coccaaaaag agaggactgt gcactagaaa gttgcagccc acagcccttc atgtggactc 540
tgtcatgaca tgctaactag acttcagggg agccacttct gttttcagcc cctccctgga 600
atagtgagtt gggaggatgg ggagacagct aaccaactgc attacccaaa ccatattgca 660
cttttagttc cctagttttc taggtgagct tcattccctg aaaggaggat gatgatatct 720
aggcataacc tagcctgtga ggaacctagt taggaaagac aactgacatt tattgaatat 780
catgcactag tecettacat atgteatatt ttaattatag aaateagtag caaaaagaat 840
cttggggatt ttccatctga cttccctggc catcttatcc catccttgca ctaccagaag 900
atteatacae ttttgagaet ceagtgagae getgttttea eccetteete etectageet 960
gggccggccg gtgggtggtc
                                                              1040
```

- (2) INFORMATION ON SEQ ID NO. 106:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1336 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```
cgagggacag aacctggtgc aggaggagtt ggcggcccgc gggacccagc ccccgtccat
ccgcaacggc ctggacaaag ccgcgaggtc cgcttcgagc gagctgagca ggccctgcgc 120
eggttcagec agggccccac accegetgec getgtccccg agggcacggc agecgagggc 180
gctcccaggc aggaaaactg tggtgcccag caggtccccg caggccgggc actagcaccc 240
ctcccagcag ccccgtgcgg acctgcgggc ccctgacgga tgaggacgtg gtcaggctgc 300
ggccctgtga gaagaagcgg ctggacatcc gtggcaaact ttacctggcc cccctcacca 360
cgtgtgggaa cctgcccttc cgacggatct gcaagcgctt cggggcggat gtgacatgtg 420
gagagatggc cgtctgcacc aacctgctgc agggccagat gtccgagtgg gccctactca 480
aacgccacca gtgtgaggac atctttggcg tccagctgga gggcgccttc cccgacacca 540
tgaccaagtg tgccgagctg ctgagccgca ccgtggaggt ggactttgtg gacatcaacg 600
teggetgece categacete gtgtacaaga agggtggggg etgtgecete atgaateget 660
ccaccaagtt ccagcagatc gtccgtggca tgaaccaggt gctggatgtg ccqctqactg 720
tgaagatccg cacaggcgtc caggagcgtg tgaacctggc gcaccgcctg ctgcccgagc 780
tgcgggactg gggcgtggca ctcgtcacgg aaatggggac atcttgtcat ttgaggatgc 840
caaccgcgcc atgcagactg gtgtcaccgg gatcatgatt gcccgtggcg ccctgctcaa 900
gccgtggctc ttcacggaga tcaaggagca gcggcactgg gacatctcgt cgtccgagcg 960
cctggacatc ctgcgggact tcaccaacta cggcctggag cactggggct cggacacgca1020
gggcgtggag aagacccggc gctttctgct cgagtggctg tccttcctgt gccggtacga1080
toccgtgggg ctgctggagc ggctcccaca gaggatcaac gagcggccgc cctactacct1140
gggccgcgac tacctggaga cgctgatggc cagccagaag gcagccgact ggatccgcat1200
cagegagatg etecttggge cagtgeece caectegeet tettgeegaa geacaaggee1260
aacgcgtaca agtagcctca ggctttccca ggggcaccct ggggcgagga gagtacaata1320
aattttattc ttttaa
                                                                 1336
```

- (2) INFORMATION ON SEQ ID NO. 107:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 812 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

ggcagcccaa tgtctcctgc acgtgcaatg caaacgctct ttgttccaga gcatggagat 60 cacggagetg gagtttgttc agatcatcat catcgtggtg gtcacgtgcc tgctgagcca120 ctacaagctg tctgcacggt ccttcatcag ccggcacagc caggggcgga ggagaaga180 tgccctgtcc tcagaaggat gcctgtggcc tcggagacac agtgtcaggc aacggaatcc240 cagageegea gtettaegee eegeetegge ceaeegaeeg eetggeegtg egeeettege300 ccagcggage gttttccacc gttgccagcc caatgtctcc tgcacgtgca actgcaaacg360 ctctttgttc cagagcatgg agatcacgga gctggagttt gttcagatca tcatcatcgt420 qqtqqtcacq tqcctqctqa qccactacaa qctqtctqca cqgtccttca tcaqccqgca480 cagccagggg cggaggagag aagatgccct gtcctcagaa ggatgcctgt ggccctcgga540 gagcacagtg tcaggcaacg gaatcccaga gccgcaggtc tacgccccgc ctcggcccac600 cqaccqcctq qccqtqccqc ccttcqccca qcqqqaqcqc ttccaccqct tccaqcccac660 ctatccgtac ctgcagcacg agatcgacct gccgcccacc atctcgctgt cagacgggga720 ggagcccca ccctaccagg gcccctggac cttcaaggtt cgggaccccg aggaggagtt780 ggaaattgaa cggggattgg gtgcggagac cc

- (2) INFORMATION ON SEQ ID NO. 108:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2681 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN: (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```
qatqcttqqt atcatcatca tgatqacqct qtqtqaccaq qtqqatattt atqaqtqcct 60
cccatccaag cgcaagactg acgtgtgcta ctactaccag aagttcttcg atagtgcctg 120
cacqatqqqt gcctaccacc cqctqctcta tqaqaaqaat ttqqtqaaqc atctcaacca 180
qqqcacaqat qagqacatct acctqcttqq aaaaqccaca ctqcctqqct tccqqaccat 240
tcactgctaa gcacaggctc ctcactcttc tccatcaggc attaaatgaa tggtctcttg 300
gecaceccag cetgggaaga acatttteet gaacaattee ageetgetee tittacteta 360
ggggcctctg tcagcaagac catggggact tcaagagcct gtggtcagga aatcaggtcc 420
agcettecet gtagecagae agtttatgag eccagageet eetgecaeae acatgeaeae 480
atatctagca ttctttccag acagcatcct ccccgccttc caccttggta gatgcaaggt 540
ctatctctcc catcagggct gccaaagctg ggctttgttt ttcccagcag aatgatgcca 600
ttctcacaaa ccaatgctct atattgcttg aagtctgcat ctaaatattg atttcacgtt 660
ttaaaqaaat tctcttaaat tacaattgtg cccaatgcag ggtqgctctg ggqqqcaaqt 720
aggtqqtaca qqqqattqqa aacatqctcc qcqcctccaq aqaaaagttq ctcccqaqqt 780
ccatgcccct ggaacgtgtt cctatcactc tggctggttg ggctggtcct tagactgggt 840
gettatgatt aaagggtett ggttageeca ettteeetet eeatgtggag atggaaggta 900
qaqaaqqata cagtgtctat cctcaagttg ctacggttca gtgaqagagg cagacatctg 960
aacaggcagg taggattcag tgtgctcagt gcactgggga tttggagaga gatgggcttg1020
ctctctctgt gcacccagga gggccacgca cttaaaactg tgtttgtgga tcagagaagg1080
ctttatagca cagggggcat tcagatgagt cttagaggaa gagaagaaac atggcaagcal140
gattacatct gagccgtttg aattgtgttt ttctttcttc ccatgtttat tttctaagat1200
ctacctgaac ttagagactc aagatatttt tttaggaaac ctcctaccca tgtctgaggt1260
agcaagtgca gcctcacgac agataccagg caatccagag ccacaaaacg tgattcctcc1320
aggetetgee tggcetgace etgteetgte agetgggttt acataceagt eccattette1380
cttttcaata aataccccca aatcttctcc taaccaccat taaagcattt tttgctttaa1440
aagcatectg acceeaattt etttgagete acgggeettt tgetgaaggt eteteagggt1500
gtagtggtgt ggctctctgg acttaacgtc actctcagag gtcagaacct tggagatcag1560
aactgattet caccaggtgt gagaggtgtg gtagcagatt gcaatgetet gcaectette1620
cttgcaagtg agcaacttca ggctctctgg gcagaggctg gcccactgta gtttgcagac1680
atgctctcca gatggtttta ctaagtcccc tctccctgat agggaatcct gctggaccag1740
cgcagcctgg gtgtggagag gttaaaagac ttgcacagga tcaccaagtc atgctgtaga1800
gccaggattc ctagacccag ggctctgcac tctcaaggct ggccccatgt gctcaagggg1860
atctaatgtt tgggctccaa actaaccatc tcggagctgg gctcctcatt tactgccaaa1920
ccctcagctt atgtagctag aaagggccct ggagtgagaa agcctggatt ttcaaattga1980
tgctccccta ctgactagct gtgccactct gggcaaatgc tcttccttga gcctgtttcc2040
acacctgtaa agtggggatg atgatcctat ctcactgctt ttgtgaggat tacaggaaag2100
cacctgtcct ggctctgtac ctggcacgta gtaggtgctc agttcatgct ggtttccttc2160
ctgcctttag tagggacctg ctctgtgctc acacctcggc tgcatgcacc ctgctgtgac2220
ggaggctagt gtggaagagg tcctgtcctc agggaattaa ctgtcttatt gggagacaac2280
aactgtcctc cttggaacac ccaagaaacc atgcaaagca gtggacaaca cagaacacgc2340
cctcctcctc gctgcctgca gctccaatct gattctgctt gggaatgggc ggagcacgtg2400
ggctgcttaa ctgctgtata ggacaagccc cttacccctc tctgggccca tgaattcctg2460
gcttggttta tgttctgatt tgacacactg attttaatct tcgaatcatg acactgagtg2520
cagaggaggt ggcattccga cagcaggaca tacatgttgg tgtgaagact gggacgacac2580
tgggtagaat ctagttttta attattatta atataaagga tcaaattaat ttaaatatga2640
atccgaagtc cacagaactt taagtgctgt gccggccatg t
                                                                  2681
```

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1407 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```
cttgggacgg aagcctagct gggtgggggg cgccgggctg gagccttcgc aggggagcgg
geteagteat caecetgege eccagagtga etcageecee aegteeceae ecateecegg 120
ggagccaggg ccgcagaggg aggtagataa gtggggtggc agcctgggtc ggccagagag 180
ttcaggccac cccggccgga cgcctgccac ttgctgtcac tgtgccgctg tcatggcacg 240
ctccgggagt gccacgccac ctgcccgggc tccgggagcc cctccacgga gcccacccca 300
gaggetggta caggatgtca gtgggecect gagggagetg egecetegge tetgecacet 360
gcgaaaggga cctcagggct atgggttcaa cctgcatagt gacaagtccc ggcccggcca 420
gtacatecge tetgtggace egggeteace tgeegeeege tetggeetee gegeeeagga 480
coggeteatt gaggtgaacg ggcagaatgt ggagggactg egecatgetg aggtggtgge 540
cagcatcaag gcacgggagg acgaggcccg gctgctggtc gtggaccccg agacagatga 600
acacttcaag cggcttcggg tcacacccac cgaggagcac gtggaaggtc ctctgccgtc 660
accogtcacc aatggaacca goodtgooda gotcaatggt ggotctgoot gotcgtoocg 720
aagtgacctg cctggttccg acaaggacac tgaggatggc agtgcctgga agcaagatcc 780
cttccaggag agcggcctcc acctgagccc cacggcggcc gaggccaagg agaaggctcg 840
agccatgcga gtcaacaagc gcgcgccaca gatggactgg aacaggaagc gtgaaatctt 900
carcaactte trageceett cetreette terggaceet graceette eegeacrage 960
cttgggcctc agcctgcccc gagctccccc agcctcagtg gactggaggg tggtcctgcc1020
attgcccaga aatcagcccc agccccggtg agcccccatc ctgcccctgc ccaccaggta1080
ctgggggcct gtggcagcaa gataggggga gagagaccca gagatgtgag agagagtcag1140
cgcgcggcag ccgcggggcg agggcctttg ctgctctgcc ggggcctgct gactgaaagg1260
aatttqtqtt tttqcttttt ttccaaaaaq atctccaqct ccacacatqt ttccacttaa1320
taccagagae ecceeegte aaageeeeee teeeeggeee ettgggaege getetaaata1380
                                                              1407
attgcaataa aacaaacctt tctctgc
```

(2) INFORMATION ON SEQ ID NO. 110:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1376 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```
cgaagaagcc ccgccccgtc ccgcttagac aatgccccgg agccgccaga ccgtcgcgcc 60
cctgccccat cgtagtatat gagctcgcct acacaaggac ccccgctaaa agccagagct 120
cccagtcccc gaggettgaa gacggggact cccttctcca ccaactctgt cctcgggggg 180
tggggcccca gccgagatca cagcgcgaca ggagtggggg tggccgctgg agacaggtga 240
ggacgccggg ggaggggctg ggccgctgct cccatgccct gatccgggga gtcccagaga 360
geotggegte gggggaaggt gegggggetg geetteeege tetggatetg gecaaagete 420
aaagggagca cggggtgctg ggaggtaaac tgaggcaacg actggggcta cagctgctag 480
aactgccacc tgaggagtca ttgccgctgg gaccgctgct tggcgacacg gccgtgatcc 540
aaggggacac ggccctaatc acgcggccct ggagccccgc tcgtaggcca gaggtcgatg 600
gagtccgcaa agccctgcaa gacctggggc tccgaattgt ggaaatagga gacgagaacg 660
cgacgctgga tggcactgac gttctcttca ccggccggga gtttttcgta ggcctctcca 720
aatggaccaa tcaccgagga gctgagatcg tggcggacac gttccgggac ttcgccgtct 780
ccactgtgcc agtctcgggt ccctcccacc tgcgcggtct ctgcggcatg gggggacctc 840.
geactiftigt ggcaggcagc agcgacgctg cccaaaaggc tgtccgggca atggcagtgc 900
tgacagatca cccatatgcc tccctgaccc tcccagatga cgcagctgct gactgtctct 960
ttettegtee tgggttgeet ggtgtgeece ettteeteet geacegtgga ggtggggate1020
tgcccaacag ccaggaggca ctgcagaagc tctctgatgt caccctggta cctgtgtcct1080
gctcagaact ggagaaggct ggcgccgggc tcagctccct ctgcttggtg ctcagcacacl140
gcccccacag ctgagggcct ggccttgggg tactgctggc caggggtagg atagtatagg1200
aagtagaagg ggaaggaggg ttagatagag aatgctgaat aggcagtagt tgggagagag1260
cctcaatatt gggggaggg agagtgtagg gaaaaggatc cactgggtga atcctcctc1320
```

- (2) INFORMATION ON SEQ ID NO. 111:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 854 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

- (2) INFORMATION ON SEQ ID NO. 112:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1681 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```
ttcagctttt gccgaaatgg gtagtgatca cacacagtca tctgcaagca aaatctcaca 60
agatgtggac aaagaggatg agtttggtta cagctggaaa aatatcagag agcgttatgg 120
aaccctaaca ggcgagctgc atatgattga actggagaaa ggtcatagtg gtttgggcct 180
aagtettget gggaacaaag accgatecag gatgagtgte tteatagtgg ggattgatee 240
aaatggagct gcaggaaaag atggtcgatt gcaaattgca gatgagcttc tagagatcaa 300
tggtcagatt ttatatggaa gaagtcatca gaatgcctca tcaatcatta aatgtgcccc 360
ttctaaagtg aaaataattt ttatcagaaa taaagatgca gtgaatcaga tggccgtatg 420
tectggaaat geagtagaae etttgeette taaeteagaa aatetteaaa ataaggagae 480
agagccaact gttactactt ctgatgcagc tgtggacctc agttcattta aaaatgtgca 540
acattetgga getteecaag gaggeagggg ggtttgggta ttgetateag egaagaagat 600
acactcagtg gagtcatcat aaagagctta acagagcatg gggtagcagc cacggatgga 660
cgactcaaag tcggagatca gatactggct gtagatgatg aaattgttgt tggttaccct 720
attgaaaagt ttattagcct tctgaagaca gcaaagatga cagtaaaact taccatccat 780
gctgagaatc cagattccca ggctgttcct tcagcagctg gtgcagccag tggagaaaaa 840
aagaacaget eccagtetet gatggteeca eagtetgget ecceagaace ggagteeate 900
cgaaatacaa gcagatcatc aacaccagca atttttgctt ctgatcctgc aacctgcccc 960
attatccctg gctgcgaaac aaccatcgag atttccaaag ggcgaacagg gctgggcctg1020
agcatcgttg ggggttcaga cacgctgctg ggtgccatta ttatccatga agtttatgaa1080
gaaggagcag catgtaaaga tggaagactc tgggctggag atcagatctt agaggtgaat1140
ggaattgact tgagaaaggc cacacatgat gaagcaatca atgtcctgag acagacgcca1200
cagagagtgc gcctgacact ctacagagat gaggccccat acaaagagga ggaagtgtgt1260
gacaccctca ctattgagct gcagaagaag ccgggaaaag gcctaggatt aagtattgtt1320
ggtaaaagaa acgatactgg agtatttgtg tcagacattg tcaaaggagg aattgcagat1380
gccgatggaa gactgatgca gggagaccag atattaatgg tgaatgggga agacgttcgt1440
aatgccaccc aagaagcggt tgccgtttgg ataaaagtgt ttccctaggg cacagttaac1500
cttqqqaagt tqgqaaggat tcaaagctgg gtcccgttcc gtttcaggag gagggagggc1560
cgtttttcaa aggcagccca gggttgagtt tgaaggggca gcctctttcg tctttttca1620
cgtttttccc acttttttgg ggatccccgt ttacattttg agttccactt ggggaagtta1680
```

(2) INFORMATION ON SEQ ID NO. 113:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ggcaatttce gttaggtget gaaggetgtg gegegeget gteeceatte ceaegtgaag 60 egetacgeta geategeteg getggeget eeeagetege egeggageag teeeggeage120 agegggggae eggaagtge teggeggget teagaageta gteeeggage eeggegtgtg180 gegeetegga geaeggtgae ggegeeatgt eeetaatetg eteeatetet aaegaagtge240 eggageaeee atgtgtatee eetgteeta ateatgttta tgageggegg eteateggag300 agtacattge ggagaatggt aeegaeeea teaaeaeea geetetetee gaggageage360 teategaeat eaeeeaatee ggeeeaatge teeeteagee aeeageatee420 eggeeattet gaaagetttg eaggatgagt gggatgeagt eatgetgeae agetteaete480 tgegeeagag eteategee gteteaeea geetetgtaee ageaegatge540 egeetgeegt gteattgee gteteaeea ggaaaetgtg aaggggatgg geaggaggge600 ttgtgeaggg ttttgtaage agtgatetag ttteattaaa aaaagaaaae aataaaaaag660 eeetgeaeae eeeteteeet teetgtegtt eaatggaeg ggtggtgget720 gtteeaeae eattttgttg eagtteetgt gagaeaggag aggetgagee aggtgaaetg780 aggaagggat gggeaggagg gettgteaa gettttgtaa geagtgatet agtteeatta840 aaaaaaagaga ae

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1739 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ttcacggatg cggacgacgt agccatcctt acctacgtga aggaaaatgc ccgctcgccc 120
ageteegtea ceggtaacge ettgtggaaa gegatggaga agageteget cacqeageac 180
tegtggcagt ceetgaagga eegetacete aageaeetge ggggecagga geataagtae 240
ctgctggggg acgcgccggt gagcccctcc tcccagaagc tcaagcggaa ggcggaggag 300
gaccoggagg cogoggatag oggggaacca cagaataaga gaactocaga tttgcctgaa 360
gaagagtatg tgaaggaaga aatccaggag aatgaagaag cagtcaaaaa gatgcttgtg 420
gaagccaccc gggagtttga ggaggttgtg gtggatgaga gccctcctga ttttgaaata 480
catataacta tgtgtgatga tgatccaccc acacctgagg aagactcaga aacacagcct 540
gatgaggagg aagaagaaga agaagaaaaa gtttctcaac cagaggtggg agctgccatt 600
aagatcattc ggcagttaat ggagaagttt aacttggatc tatcaacagt tacacaggcc 660
ttcctaaaaa atagtggtga gctggaggct acttccgcct tcttagcgtc tggtcagaga 720
gctgatggat atcccatttg gtcccgacaa gatgacatag atttgcaaaa agatgatgag 780
gataccagag aggcattggt caaaaaattt ggtgctcaga atgtagctcg gaggattgaa 840
gttaaaaaaa attgtgacca atgaacttta gagagttctt gcattggaac tggcacttat 960
tttctgacca tcgctgctgt tgctctgtga gtcctagatt tttgtagcca agcagagttg1020
tagaggggga taaaaagaaa agaaattgga tqtatttaca qctqtccttq aacaaqtatc1080
aatgtgttta tgaaaggaag atctaaatca gacaggagtt ggtctacata gtagtaatcc1140
attqttggaa tggaaccctt gctatagtag tgacaaagtg aaaggaaatt taggaggcat1200
aggccatttc aggcagcata agtaatctcc tgtcctttgg cagaagctcc tttagattgg1260
gatagattcc aaataaagaa tctagaaata ggagaagatt taattatgag gccttgaaca1320
eggattatee ecaaaceett gteattteee ecagtgaget etgattteta gaetgetttg1380
aaaatgetgt atteattttg etaaettagt atttgggtae eetgetettt ggetgttett1440
tttttggage eetteteagt caagtetgee ggatgtettt etttacetae eeeteagttt1500
toottaaaac gogcacacaa ototagagag tgttaagaat aatgttactt ggttaatgtg1560
ttatttattg agtattgttt gtgctaagca ttgtgttaga tttaaaaaat tagtggattg1620
actccacttt gttgtgttgt tttcattgtt gaaaataaat ataactttgt attcgaaaaa1680
aaaaaaaaa aaaaaaaaag gaggagaaaa agaggggaaa gggggaagag gagcaaaga 1739
```

- (2) INFORMATION ON SEQ ID NO. 115:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 805 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

- (2) INFORMATION ON SEQ ID NO. 116:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1483 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```
tgaaaaagac ccaacgccaa cacctggtgc cttttgcagc cagcgcccac ccatccgtgc 60
coggaccett gggaatgeec geggeteeag aggaaaaage ccagggaegg ggeeteegtt 120
gegggggte ggetgettet tgggaacttt gtegttteeg gegetggetg getggetgge 180
tgtaaagcac tgaagccccc cggccgccaa cccctgaaag cagaacctgg cctccctggc 240
cacageagee traceaceg cretaegtgt ecegggeact tecegeagee treeegreee 300
ttteteateg geettgtagt tgtacagtge tgttggtttg aaaaggtgat gtgtggggag 360
tgcggctcat cactgagtag agaggtagaa tttctattta accagacctg tagtagtatt 420
accaatccag ttcaattaag gtgatttttt gtaattatta ttattttggt gggacaatct 480
ttaattttct aaagatagca ctaacatcag ctcattagcc acctgtgcct gtccccgcct 540
tggcccggct ggatgaagcg gcttccccgc agggccccca cttcccagtg gctgcttcct 600
ggggacccag ggcaccccgg cacettcagg cacgctcctc agetggtcac ctcccggctt 660
tgccgttcag atggggctcc tgaggctcag gagtgaagat gccacagagc cgggctcccc 720
taggetgegt egggeatget tggaagetgg cetgeeagga cetteeacce tggggeetgt 780
gtcagccgcc ggccctccgc accctggaag cacacggcct ctgggaagga cagccctgac 840
cttcggtttt ccgagcacgg tgtttcccaa gaattctggg ctggcggcct ggtggcagtg 900
ctggagatga eccegagece eteccegtgg ggcacecagg agggeeetge eggaatgtge 960
agcctgtggg tagtcggctg gtgtccctgt cgtggagctg gggtgcgtga tctggtgctc1020
gtccacgcag gtgtgtggtg taaacatgta tgtgctgtac agagagacgc gtgtggagag1080
agccgcacac cagcgccacc caggaaaggc ggagcggtta ccagtgtttt gtgtttattt1140
ttaatcaaga cgtttcccct gttttcctat aaatttgctt cgtgtaagca agtacataag1200
gaccetectt tggtgaaate egggttegaa tgaatatete aaggeaggag atgeatetat1260
tttaagatge tttggageag acagetttag cegtteecaa teettageaa tgeettaget1320
gggacgcata gctaatactt tagagaggat gacagatcca taaagagagt aaagataaga1380
gaaaatgtct aaagcatctg gaaaggtaaa aaaaaaaaa tctatttttg gacaaatgta1440
attttatccc ccatgggatg cttgggtatg gcgggggga ggc
                                                                 1483
```

- (2) INFORMATION ON SEQ ID NO. 117:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1347 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - -
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

tgaggtcttc catgactgca agtgttatat tggactggat ggtcatgaag tccctttcat agccagagat tttgtgtggc tgctaaaatg cttacatctc tggctatgaa agggacttca 120 tgaccatcca gtccaatata acacttgcag acagagaaac tgaggtcttc catgacttgc 180 ctagtctccc agctagtttg aggcaaaact ggattcccac tctggtattc tttcttccct 240 ttacatcatt ttccctcctt tataatgtcc tgagagacca gaactcacac cagaatcgat 300 tattcctcag gtgaagcata gactctttca tggtagacag atttcacgac tcagagatag 360 aaatctcttg ctatcatcag gtcacgggca gctcctgtgg agtcctgccc aacttatgtg 420 gcttccataa aatggcaaca gtccaggctc cttgcctaat tttagagcat taactcccta 480 attgccagta agcaaggagg tggatctctg caaacctaca ctgtctatga cagctctagt 540 tgtacttggt gtgactaaat acctcaaagg caacctgctt ctgcaggttt tgaagtgtca 600 gcttcataag acactgaggt ttagaattgt ttgattctag accataactg aagggcataa 660 atggaaacag gatatgaagg gaaacaagta gcatcatgga gctgaaaagt ggtgcatcac 720 ccaatggcta gcacaaacaa ggatcacact gtccattctc ttgtctgcta aattaagcat 780 tttcttgcct cctttgcttc atcttttcac aacagctgga tagagggatc agaaatgact 840 gtgtcatggt gctcattcac tgcaaactcc cagttgcaag ctccttggct cccccggagg 900 gagcaagaat ctcatagttc agagacacag agggcctttt agccctaatg accttttgga 960 tgggactgca actcatgact atcctgatat tggaagaaag gactttgtta atcttctccc1020 ccatagetet getgegtagg tetacatett acteagaate actacaeatt cetttagtet1080 tcctccaage tccagageca ttggtacaaa tgctttattg aaactaaata cataatacac1140 acaatgagat gaagacaata tagaagtccg catagtcatc ataatcccgt tccttggccg1200 gttgaggcag ctcagtggct gagcccagtc aagccaaccc gcagcttcac tcacgacttc1260 aagatttgat gctaattctt ttggatttct acagttatta aataagtgtc tgagtggaaa1320 aaaaaaaaaa aaaaaaaaa aaaaaat 1347 .

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1683 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```
aattcggcac gatgggggga atctccgacc ccgacaccct acacatctgg aagaccaaca
                                                                   60
geetteetet eeggttetgg gtgaacatee tgaagaacee eeagtttgte tttgacateg 120
acaagacaga ccacatcgac gcctgccttt cagtcatcgc gcaggccttc atcgacgcct 180
getecatete tgacetgeag etgggeaagg attegeeaac caacaagete etetacgeea 240
aggagattee tgagtacegg aagategtge agegetaeta caageagate caggacatga 300
cgccgctcag cgagcaagag atgaatgccc atctggccga ggagtcgagg aaataccaga 360
atgagttcaa caccaatgtg gccatggcag agatttataa gtacgccaag aggtatcggc 420
cgcagatcat ggccgcgctg gaggccaacc ccacggcccg gaggacacaa ctgcagcaca 480
agtttgagca ggtggtggct ttgatggagg acaacatcta cgagtgctac agtgaggcct 540
gagacacatg gagagttggt caggctgctg ctgggagaaa tggacgccca ctgggcctca 600
acttgatctt ctaccccgtg cctgtgactc agactgggaa atactgagca gagacggctg 660
gggcgggggc aggaggaggg gctgctctct gagacagggg cgcccccgcc ttgacccctg 720
ggcaceteca teccetecca ectgtececa gateagtete tgggatggag gecagagage 780
tggtcaggct cccccatctg cccagcacgg cctgcactgt gcccacccac ttgctccaca 840
acqtccagtt ggtcctgctg ccaagagccc cgtgcatcca ggcggccaag cacaaactgg 900
gggagaggag geogecagee eggaggetge ageccagaaa etetacetea tecacactgg 960
tgcagggage ceteettgaa etgacetttg attggtttet getteaacta ceaaaatgtt1020
atotocactt cocceteace egtagaggat cetggecaca gacagtttea agtagtgtcal080
gatttttgtt gcttgggcgg ctgttggtag agtgggcagt gcccgcgcca tggggtgctc1140
tgtgggcttc tccaggagca gggagggtgg aggggaggga tggggggcac aggagctggg1200
agccccgtct ccaggaaaag gagaggggtt aagatgcacc gaggctgtag ctgggctact1260
tgatcttgct gaaagtgttt ctaaagatag caccactttt ttttttaaag cttttatata1320
ttaaaaaacg tatcatgcac caactgtgaa tagctgccgc ttgcgcagag gacccgggga1380 ....
ggggtcccga gaggctcccc atgcaacact ggaaatgact gttccagaga gcgggcagac1440
ctggcagage gcccctggcg cctgagacta ccacccactc cgttcctgcc agaaacgacc1500
ctctgtggcc gatgggccat gcgggccct cgcagccaac tcagccagtg ttgggactgg1560
ctcagagccc atgggggctg gagggggca gctgggactc tggaatcttc tttataataa1620
aagccttacg gacaaaccta aaaaaaaaa aacaagacaa gagagggaaa gggaaagaag1680
ggg
                                                                 1683
```



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1355 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```
acaagcatgg aagctttact gtttcggctc ttcaaacttc cagcaactac actgcggtgc
atoggaette gaegeeeget ggtgaegeae aegetgegee ggaagtgtga acacaaagee 120
tccaggettt gtcatggegg etgetgetge acgetggaac catgtgtggg tcggcaccga 180
gactgggatc ttgaaagggg taaatcttca qcgaaaacag gcggcgaact tcacggccgg 240
aggacagecg eggegegagg aggeagtgag egecetgtgt tggggcaeeg geggegagae 300
ccagatgctg gtgggctgcg cggacaggac ggtgaagcac ttcagcaccg aggatggcat 360
attecagggt cagagacact gcccgggcgg ggagggcatg ttccgtggcc tcgcccaggc 420
cgacggcacc ctcatcacat gtgtggattc tgggattctc agagtctggc atgacaagga 480
caaggacaca teetetgace caeteetgga actgagagtg ggeeetgggg tgtgtaggat 540
gegecaagae ceageacae cecatgtggt tgccacaggt gggaaagaga atgetttgaa 600
gatatgggac ctgcagggct ctgaggaacc tgtgttcagg gccaagaacg tgcggaatga 660
ctggctggac ttgcgggttc ccatctggga ccaggacata cagtttctcc caggatcaca 720
gaagettgte acctgcacag ggtaccacca ggtccgtgtt tatgatccag catccccca 780
gegeeggeea gteetagaga eeacetatgg agagtaceea etaacageea tgaceetcae 840
teegggagge aacteagtga ttgtgggaaa caeteatggg cagetggeag aaattgaeet 900
toggcaaggg cgtctactgg gctgtctgaa ggggctggca ggcagtgtgc gtgggttgca 960
gtgccaccct tcaaagcctc tactagcctc ctgtggcttg gacagagtct tgaggataca1020
caggatccag aatccacggg gtctggagca taaggtttat ctcaagtctc aattgaactg1080
cctcctcttg tcaggcaggg acaactggga ggatgagccc caagagcctc aagaacccaal140
caaggtgccc ctagaagaca cagagacaga tgaactttgg gcatccttgg aggcagctgc1200
caageggaag ctetegggtt tggageagee ceaaggaget etecaaacga gaeggagaaa1260
gaagaagegg cetgggteea ceageceetg acgeeeetgt geeeactttg taaataaact1320
gctgaacacc caaaaaaaa gaaaaaaaa agggg
```

(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1816 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```
ggtcagagag attctgaaaa gtaatccaaa gtgttccgta gctaaacatg gtgcaggctc 60
gttgtaccac tgcaaccgac tgacgttact gtagttccta gaatgctgtg agggcggggg 120
gttcagatca acataaagcc taacttgctg gagttgtagt ctcaaggctt tctctcttgc 180
ttaactaaaa cctaaggacc actgtttttg gtagcaatta tatggttact atccactgca 240
gtcctcagtt gttggggtaa atcccacatg gcagagtaag gcaccccaca gaaattaact 300
tggagagect gagaaattee cagtggeett ggeatagetg tetagaacae catetetagg 360
aaaatttaat totgtooctg gocagotatt gttottooac ttogttttot gotgtoocaa 420
ggccagatga gtggaatcac catctgactg ttgtcaataa aatgtatctg gcgtgaacag 480
caggataacc catgttetee acataaggat aaccttacgt gaaaccttee tgetgacaac 540
catgcagagg aatttttcca cttaagtcag agccttcctc cccatctgga attcacagct 600
gttccctggc agcacacagg agggtattaa ggacctttgt gaggctaggt acactgtcca 660
cacctetttg gggaagttac gattttttt ttecateata atteagtete ttettattet 720
acagtgtgca ctttatgcct ctcgcctttt gataatagtt gttcagtgaa ggaagtcagc 780
tgccagaata ttaagaaggg tctcccttta tgtcagtaca actgttaggg cggccttccc 840
atttacttta ggtttcaaga ggattcaccg gaagcacatg ccccggtcta gtcccatttg 900
aaacagttct gctttactga gaccctaggc cggtctcctt gctgacccta gcgctgctgc 960
ctaggtgcca tttcctttcc tcctcagtca aatacaggct gcacattttg tcacttaatg1020
ccagtacaat ctgtgttact cctaaggact tttgggattt tgatgagacc tgcgagggag1080
aagacactga gaagccagtg atctgcaagc atttgctctt gtttccacat cacctctgggl140
atatttcagc tgttgtttcc aaatggcaaa tcatcaacta aaagcacttg tttcaagttt1200
tgttctgcac tcccacgact gaagttgtag attgagctga ataaccatgg gaagtgaccal260
agcaaagaca ctcgattgga gtcagttgaa tatttgtacc ctcagtggag cccttctggt1320
cttttcttcc acttctgcag aatttcctct agcaaatact tctttctcct tgcttccctc1380
caccatgata tttgaataag agatggccag aggataacac ttgtctctta aaaactaagc1440
taaaaagaac ctagaacctt caattgagca gttgtgaaaa ttgctaatgg tgccaaggcc1500
aagcaaagag tttcagaaaa tgactgagaa ggagcgataa cccccagaat gcaaaatcag1560
gggcatcatt atccggtgct tgaacaagga gctccgctct acaactggtt tttttaggac1620
ttgtgaggaa cacagcaacg gaaatccatc cacaaaggat gcagtgcccc aacttgtact1680
gcgcctgaat agtcatgtga taatttactg aagaaatcta gtgtacttta aattttttc1740
ataaaagttt acattgtatt gtaggttaac attaaatgtt ttatagcaaa aacttcaaaa1800
aaaaaaaaa aaaaaa
                                                                 1816
```

- (2) INFORMATION ON SEQ ID NO. 123:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 740 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

tttagaattc agcataggtt gaggtcagaa agcaattcag gcatgagcca ccgtgcccgg 60 ctccacaccc atttcttaa aaaggatccc gtagcaggca gaaaagcccc ttccatcctg120 ctcctctgat actgtgcccc cttggagata tttccgtcct ccacccacgt gtctgtggct180 ggaactgccc agcctgccc tggcccctg gaagcctccc cacagctggt aatctggact240 taaggattgc tgggccaccg cctctctgcc taccaccatt ccatatttaa gtggagcccc300 tacgtagaaa ggccccgggg ctttatttta gtctcctttt cagggatgtc gtggggggg360 gagggggttc ttggtgctac agccctctcc ccacccctaa agggacgccg acgctgtttg420 ctgccttcac cacatattag tgcttgaccc tggcagggga ccccatggaa aagatgggga480 agagcaaaat acatggagac gacgcacct ccaggatgct cgctgggatt ccccacgag600 cgaataaagc caaggcttct tcccaaaaaa aaaaaaaaa aaaaaaaaa aagataggtt660 agttaaggcg gccgaaagtt tttttccctt tagtaagggt tagttttag tttggggttg720 gccttcgttt ttaagaacgt

- (2) INFORMATION ON SEQ ID NO. 124:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1493 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```
aacacctgcc ctcgttcagc gctttaggga gggcggctca ggcgccccgg agcaggcaga
gtgcgtggag ctgctgctgg ccctgggcga gcctgcggag gagctgtgcg aggagttcct 120
ggcgcacgcc cgcggccggc tggagaagga gctgagaaac ctggaggccg agctggggcc 180
ctcacctccg gctcccgacg tgttagagtt caccgaccat ggaggcagtg gcttcgtggg 240
eggeetetge eaggtggegg eggeetacea ggagetgttt geggeecagg geecageagg 300
tgccgagaag ctggcggcct tcgcccggca gctgggcagc cgctattttg cgctggtgga 360
geggeggetg gegeaggage agggtggtgg tgacaactea etgetggtge gggegetgga 420
cogettecae eggegettge gggetecegg ggecetgetg geogetgeeg ggetegeaga 480
cgctgccacg gagatcgtgg aacgagtggc ccgcgagcgc ctgggccacc acctgcaggg 540
teteegggeg geetteetgg getgeetgae agaegteege eaggegetgg eageaeeteg 600
cgtggctggg aaggaggcc ctggcctggc cgagttgctg gccaatgtgg ccagctccat 660
cetgagecae attaaggeet etetggeage agtgeaeett tteacegeea aagaggtgte 720
ettetecaae aageestaet teeggggtga gttetgeagt cagggtgtee gtgagggeet 780
categtggge ttegtecact etatgtgeea gaeggeteag agettetgeg acagecetgg 840
ggagaagggg ggtgccacac cacctgccct gctcctgctg ctctcccgcc tctgcctgga 900
ctacgagacg gccaccatct cctacatcct cactctcact gatgaacagt ttctggtgca 960
ggatcagttc ccagtgacgc ccgtgagcac gctgtgtgca gaggccaggg aaacggcgcg1020
geggetgetg acceactacg tgaaggtgea gggeetggte atateaeaga tgetgegeaa1080
gagcgtggag actcgcgact ggctcagcac tctggagccc cggaatgtgc gggccgtcat1140
gaagegggtg gtggaggata ceacegeeat egaegtgeag gtggggetee tgtacgaaga1200
gggtgttcgc aaggcccaga gcagcgactc cagcaagagg actttctccg tgtacagcag1260
ctctcggcag cagggccgct acgccccag ctataccccc agtgccccga tggacaccaa1320
cctcttgagc aatatccaga agctattctc tgaacgtatt gatgtgttca gccctgtgga1380
gttcaacaag gtgtcggtgc tgaccggcat catcaagatc agcctgaaga cgcttgctgg1440
gagtgtgtgc gggctgcgaa cctttttggc cctttgcggg cttcaacaag ggg
```

- (2) INFORMATION ON SEQ ID NO. 125:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ccagactgaa ttgtcagtga gcggatctga gggcggtgtg gagtggccag tggggcttgg 60 ccgagatgga caaccggatt ccttatgatg actagccggt ggtttcttgc ctgcctatga120 ttgacccagt tttggcccga accatcacac tgaagaagcc tcctggagtc attgggatta240 agatcgaggg

(2) INFORMATION ON SEQ ID NO. 126:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
tcggggggag cggcgggcg gcgcgggagt tggttctaaa gagtggtgag tcagaagaga
cgtcaggcag caagcgactt gggccatggc ctctgaccta gacttctcac ctccggaggt 120
geoegageee actitectgg agaacetget aeggtaegga etetteetgg gageeatett 180
ccageteate tgtgtgetgg ccateategt acceattece aagteecaeg aggeggagge 240
tgaaccgtct gagcccagaa gtgctgaggt gacgaggaag cccaaggctg ctgttccttc 300
tgtgaacaag aggcccaaga aagagactaa gaagaagcgg tagaagagga ggcctgagga 360
gctgggcggg cagggagagg gtcttgggga cagccctcct gggaatctac attgtgttcc 420
ecegeattee aggeteaggg tetgaggagg etgtgaegee etatgaeege agagatetag 480
acagtogtaa cagtococag gotocagotg ggcaatocac cacttoctot toottotgot 540
tctgtgacgg tttagagtca agggggctga aacacactgt gagcatagac tgtattaggt 600
ttgttcagaa gccgggtcag ctcacagagt cacattttct tgcttagtca tgtgtccctc 660
cttgagttgc cccctccttg tgggtttaca ctacattttg gagtcattgt ctaatgctga 720
caagcacacc ctctcccatt atttgtgcac tacagatctc ctgctgatca gtcacctttg 780
ttgctgctgt gtagacagag ccaggcctca cctgtttgtt taggccaaga tgccatggac 840
atgcagegtt agtgatecca etagetgtga cagecaggee cagaaaatge etggegtgag 900
agccagcaga cagccaggcc aggggtaggc agtgcctgct tctgctccat caggtgcagg 960
ggatttggct gaaggcgtgc atatttcctg ggcacaaact tcctgagcct ctgaaatggg1020
aggetegtea atticagace aacetettit caacecatea tagcacgite aaggigtgec1080
ttttacttct acctgtacat cocccatece ttcaattctt tcattccctg accagtgagal140
gggttcctgg gggaagtatg gtgaataaac tgacatgcat gcttcagaaa aaaaaaaaa1200
```

- (2) INFORMATION ON SEQ ID NO. 127:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1014 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
cccttttttt ttcttttga gatgggggga aagtcctagc aaaaggcagg agttagcatt
ttcctttaac aagactttct aatgctaaac aaagaccaac ttcttttaaa aggggttgtt 120
ttggttgtgg gtgaaaaata ctgtactgta atgatctgct tggttttaaa gcaaaagaga 180
tectgacatg tgaaaccaat acaccaaaat gecaagteea caaatgaaca aaacaagtge 240
ttaaaaaaaa aattottotg otottatatt tttggaggaa gotgotgatt ttggotgtoa 300
gatttcactt agaaatggtc actttctgag atgctttttc ctcacagaat ctgtagataa 360
actcattaaa agattgtccc atttcaaaat cacccccaag tctagcagca ctgtttttt 420
tttttttagt ttttgtttta aaattacaaa ccaagtaaga agtccaacat cctcttccat 480
gaacagettt gtgacagage teetgagtgt gtgeageece caetgtgete tqaatacagt 540
ctctgcagct ccagtgtgtc ctcttttcag gaaggaaagc atattcaata cattcactat 600
ctgtaccccc tggaacttgc acatgctgac gagctattat aagccaactc atccccagct 660
ctcttccggg actggtcacc ccttgtaaaa ccattctgta taagttctct ttgaaatttc 720
tgatcttgag cagcatattc agaaagttca gattccaccg ccggagggag aatgtttgga 780
ataaatttag aaaatagagt tggagccatc tgaacccact ctggtctgag ggtatacagg 840
cctttcacaa tatttgccat agttgaaggt gtgacctgaa atggtgttga ctgggcttct 900
aaaagtaaag gcattaggcc gtaaatgtgc ttttctgcaa catgttccgt aaacagcttt 960
ataagggcac ctttaagccc gggtaagctg gtccatggga acctatcgtt tttq
```

- (2) INFORMATION ON SEQ ID NO. 128:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1171 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```
caccaaatta atcaggttta cagacagggt cccaccggta ttcacattct tgttagtgat
cagatggttc agaattttca agatgagagt tgttttttat tctccacagt aaaagctgaa 120
agtagtgatg gcatccacat aattttgaaa tgatgtctta tatagactga actgtattca 180
gtaccaaata gtcacgctta aaagtgtgtg aagactgaat ccaagaagtc ttgggattgg 240
attttaccat atgaaatgtt tcatattgaa aacacaagat gacctttcta atgagctgta 300
tgagaggtga atctcctcac tgtcactgcc atagccaagc atcctcatga gagtgagcac 360
ateggeacag catgeateca getetggagg ceaeggtgea ggeatagetg cetgetgete 420
tggcagaggc cagtaaatac agttcctaga agcagccttt gctgtctttt tacactgtat 480
gcggtttgga aatgaatgta gaaacttact gtgggcattt acctttctgt gccagtttgg 540
cttttattgc ctgaacctta tgctgacctg gagaggagat gggggacagt gctgttgtgg 600
ggccagcagt gaatctgtat gcggagagtt gtgttgtgct gatgtggccg ttggtggtca 660
ggtaagaggc tcggcacctt cttggaagaa atcatgtctg agggtgtacg tttgatatga 720
tcatgccaga ttggagaaga tccaagccag gaagatgggc ttgaagcaaa ctgcattatc 780
aggagtacct tggtgagagg atcagtgtaa atcctaatag gtacaaagac ttttgtgttt 840
tggctttgtc acagatttat tgaaaaactt ttttgcttct gcttccattt ttagcatttt 900
agtttctggt tttcattttt ggagattcct tgccttttaa actcgtggtt tttctctcat 960
tttcttccct ctctccctcc atctctgacc accccaccc taacccccca ccccaaccat1020
cctattaaac atttttaaag ccctacccca gacattggga aataggtgga cccaagtagg1080
gggggaggaa agtattgatt tgtttggata ggcttgtgga ttagggtgtt aaggggttct1140
tggattatgg aacaaggtgg aattttttt g
```

- (2) INFORMATION ON SEQ ID NO. 129:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```
ggccgggacg cagggcaaag cgagccatgg ctgtctacgt cgggatgctg cgcctgggga 60 ggctgtgcg cgggagctcg ggggtgctg gggcccgggc cgccctctc cggagttggc120 aggaagccag gttgcagggt gtccgcttcc tcagttccag agaggtggat cgcatggtct180 ccacgccat cggaggcctc agctacgttc aggggtgcac caaaaagcat cttaacagca240 agactgtggg ccagtgcct aggttgacct ttgcccaact caaggaggag tgg 353
```

- (2) INFORMATION ON SEQ ID NO. 130:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

cggctgagcg gccccgcagc caacccccga ggagcggccg gctggcgtgc cgctggcgcc 60 caggagttgg ggatgtccta caaacccatg cgccctggc tgcccagcag caccccctgg120 tctgccaggc accccctggg gcccggggca ccccggttcc ctgacaggga ggcgtgcgcg180 tgcgccgtgc ggggctgcag tgtcc

- (2) INFORMATION ON SEQ ID NO. 131:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 211 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

aaatcacctt acaacccatt tctcagaaca tgtttctatt gttaaacaac acacaactat 60 tttatttatg tgttttattt atgcctgatc accaatatca ataactgaaa cacagcagtt120 tagtaataat ttaatacaca ccataacctg cctattgaga atggcattat atttgttttc180 attgtagtgg ctccatccaa aataaaatga t

- (2) INFORMATION ON SEQ ID NO. 132:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 867 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

gtcttcccaa gatggagatg ctaacgaaac tgagaagggg gcgtatgttt gacgaaggtt 60 tgtgcaagtc aggcccttct ggaacacagc agggcctaca acgaggggcc tttgcgatgg120 gctgtgagga tgggggggt gggaagaatt ggccacgtta gagaccccat gccaccccac180 catggtgagt gctctgtgcc tcctgctcac ctgtggtgag tgggcgagct gggcgagctg240 ggcgagctgg gctggggaga gcctgtgagg accgagagaga gaaatgagaa gaaggaacaa300 aaatattatt tctatgtaat ttatatttta cttatgccaa attatttatg ataatttta cttatgccaa agctgtgatt ttgtgaggct420 tgtccctatg taggatgcac cgccagaggccc tggccactga aagagtgtgc agtggagctg240 gggtctccca tatgcggtgc cgcccaaagg tggctttgcc tcaagcaacc taccctgatg540 ttttactcat tggaatgtt ttccccgatt gtggatgact tctttctga tggagagagt600 catcttcagg cctgaagctg cacgacctga agttcgcctg catttatcag cctgaagctg ggttcctgc ggggaccatg tgtggttgt gcatgttga780 gcagaaggga ggatgagaa aaaagagaag gaaaccccg ttagtgacaa gtgtttttt840 gagttgccag gttttgccat cattaaa

- (2) INFORMATION ON SEQ ID NO. 133:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

aattcagact cccattctta acttggcatt tttgtagctt acaggaacca gcttggtgta 60 ccttctctta tgagatgcag ctggaaagcc atttatgcaa gaggtggttt cacttttgtc120 gctcctccat tcattgaccc ttcagccttt aaaaaaattag aatgtgaaaa ttagtagcaa180 agagtgcaga gatattagct taagggataa ataaatgaaa gtagcaagta gctcattatt240 tatgaagagt aataatt

- (2) INFORMATION ON SEQ ID NO. 134:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

gactggctca tggcctctgt aaatggctgc tggcgggact gtctgcctag cgggtgccct 60 tggaacctag cccttggtgg gttttgagga aatgattcct gaatgaggag tcgattgccg120 tgtgaagggc tggtggcacg gcacccgcgt gagctacgcg tgccctcagt gcgcttctgg180 attgactggc catgggtgct caca

- (2) INFORMATION ON SEQ ID NO. 135:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ttgcaccatg gtaaacgtgg ataatacagt atcatttttg agcagttttt taaatgtaaa 60 tctgtatctt actcagagtg tgtgtctgaa gttattaagg acatttccca acgttactgg120 cccatttccc tttgtaatca gaggaattct gtttcaagat tattgttgtg tgtgatctgt180 ggctcttgat cagaatgaag ttaaatggcc acaggaggat taagctatga ggttggcatt240 tttca

- (2) INFORMATION ON SEQ ID NO. 136:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1637 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
ggggagggac gagtatggaa ccctgaaggt agcaagtcca ggcactggcc tgaccatccg
getecetggg caccaagtee caggeaggag cagetgtttt ceatecette ceagacaage 120
tetattttta teacaatgae etttagagag gteteccagg ceageteaag gtgteccaet 180
atcccctctg gagggaagag gcaggaaaat tctccccggg tccctgtcat gctactttct 240
ccatcccagt tcagactgtc caggacatct tatctgcagc cataagagaa ttataaggca 300
gtgatttccc ttaggcccag gacttgggcc tccagctcat ctgttccttc tgggcccatt 360
catggcaggt tctgggctca aagctgaact ggggagagaa gagatacaga gctaccatgt 420
gactttacct gattgccctc agtttggggt tgcttattgg gaaagagaga gacaaagagt 480
tacttgttac gggaaatatg aaaagcatgg ccaggatgca tagaggagat tctagcaggg 540
gacaggattg gctcagatga cccctgaggg ctcttccagt cttgaaatgc attccatgat 600
attaggaagt cgggggtggg tggtggtggt gggctagttg ggtttgaatt taggggccga 660
tgagcttggg tacgtgagca gggtgttaag ttagggtctg cctgtatttc tggtcccctt 720
ggaaatgtcc ccttcttcag tgtcagacct cagtcccagt gtccatatcg tgcccagaaa 780
agtagacatt atcctgcccc atcccttccc cagtgcactc tgacctagct agtgcctggt 840
gcccagtgac ctgggggagc ctggctgcag gccctcactg gttccctaaa ccttggtggc 900
tgtgattcag gtccccaggg gggactcagg gaggaatatg gctgagttct gtagtttcca 960
gagttggctg gtagagcctt ctagaggttc agaatattag cttcaggatc agctgggggt1020
atggaattgg ctgaggatca aacgtatgta ggtgaaagga taccaggatg ttgctaaagg1080
tgagggacag tttgggtttg ggacttacca gggtgatgtt agatctggaa cccccaagtg1140
aggctggagg gagttaaggt cagtatggaa gatagggttg ggacagggtg ctttggaatg1200
aaagagtgac cttagagggc teettgggee teaggaatge teetgetget gtgaagatgal260
gaaggtgctc ttactcagtt aatgatgagt gactatattt accaaagccc ctacctgctg1320
ctgggtccct tgtagcacag gagactgggg ctaagggccc ctcccaggga agggacaccal380
teaggeetet ggetgaggea gtageataga ggatecattt etacetgeat tteecagagg1440
actagcagga ggcagcettg agaaaccggc agttcccaag ccagcgcctg gctgttctct1500
cattgtcact gccctctccc caacctctcc tctaacccac tagagattgc ctgtgtcctg1560
cctcttgcct cttgtagaat gcagctctgg ccctcaataa atgcttcctg cattcatctg1620
caaaaaaaa aattttc
```

- (2) INFORMATION ON SEQ ID NO. 137:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

aaaagcatag ctcactctgt aataggctat tttcatgatt tcaagtggtt ttatgaagaa 60 acagaaagca gtgatgatgt tgaagtgctg actctcaaga aattcaaagg agacctggccl20 tacagacgac aagagtatca ggtagaattc aacatatggt gcttgaagtg ggctcttgtt180 ttatcagtta tggcatatgt aaataacagt gtaccaagtt agtgtggtgt ttatgaagat240 gagtttaatc ttttgtgatg

- (2) INFORMATION ON SEQ ID NO. 138:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ggggaatttg tetttggaaa gettgtgeaa eetetacaae tggegataca agaatetagg 60 aaacttaccc catgtgcagc tcttgccaga gtttagtaca gcaaatgctg gcttactgta120 tgacttccag ctcattaatg ttgaagattt tcaaggagtg ggagaatctg aacctaatcc180 ttacttctat cagaatcttg gagaggcaga atatgtagta gcacttttta tgtacatgtg240 tttacttggt taccctgctg acaaaatcag tattctaaca acatataatg gccaaaagca300 tettattege gacateatea atagacgatg tggaaacaat ccattgattg gaagaccaaa360 caaggtgaca actgttgata gatttcaagg tcaacagaat gactatattc ttctttctct420 ggtacgaacc agggcagtgg gccatctgag ggatgtccgt cgcttggtag tggccatgtc480 tagagccaga cttggacttt atatcttcgc cagagtatcc ctcttccaaa actgttttga540 actgactcca gctttcagtc agctcacagc tcgcccctt catttgcata taattccaac600 agaacctttc ccaactacta gaaagaatgg agagagacca tctcatgaag tacaaataat660 aaaaaatatg ccccagatgg caaactttgt atacaacatg tacatgcatt tgatacagac720 tacacatcat tatcatcaga ctttattaca actaccacct gctatggtag aagagggtga780 ggaagttcaa aatcaagaaa cagagttgga aacagaagaa gaggccatga ctgttcaagc840 tgacatcata cccagtccaa cagacaccag ctgccgtcaa gaaactccag cctttgagcg900 tgagagccgc cccggtgggg aaggggcaat tgcgttgggg gggcttgggt gtttttt

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 760 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

- (2) INFORMATION ON SEQ ID NO. 140:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

aggaaccctc cggcctagaa gttcagatgt cttgccaata tatctgtgct tcacaacttg 60 cctactctct ctgaccccta acattttcac atacttttcc aattctgcct gtcataaatt120 tgctgcttcc ccctaagtag aatgttgatt cctgtcaaac acaaggccta gccctgattc180 ctcctcttct ctcaagcagt gatattgtca acaatgataa acaactacta tgtactgagt240 gtttttttat gtgctgctca cactttatac acatgtatag

- (2) INFORMATION ON SEQ ID NO. 142:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

geggeegete gagggaagea eeegeeggtt ggeegaagte eacgaageeg eeetetgeta 60 gggaaaacee etggttetee atgeeacaee teteteeagg tgeeetetge etetteaeee120 eacaagaage ettateetae gteettetet eeatetateg gaeeeeagtt tecateaeta180 teteteeagage tgtagetatt atgegeeggt etaeaggggg tgeeegaega tgaeggtgee240 tecgeagte aattaetett egggteeeaa ggtttggett teaegggete eattgeeeeg300 gegtggeagg eeetteeagg eeetteeggg etggaaetgg tgteggagga geetegggtg360 tategtaege eetggttg gtgttgeete aeteetetga getettettt etgateaage420 eetgettaaa gttaaataaa atagaatgaa tgataeeee g

- (2) INFORMATION ON SEQ ID NO. 143:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

caaagatgte atgtggcag aatcatett tagteteace actecacat gatggtcaca 60 tagaggtgtg agttgggaag ttgttaaata caagagggtt tgagettetg gagaagaggg120 aaatgtaaaa gtattttte etttaagaaa gataaaaagg taageetaaa eetttggegge180 cacegaagte agetgttaeg eatgtgtagt taaattteae tgtaaatatt teataagggt240 tettagaatg gagecaggtt gacateacag eeceaactgt aceaaaggaa eeattteeat aagaaacacg aatgtetatg geagagttaa eataaggtea360 gaaaateete tggaagaaat tteggtatea atgtttataa teetetgeatt taggggtttg420 eeagtttggg eaaaaa

- (2) INFORMATION ON SEQ ID NO. 144:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

ctttaaagta gggctgtgga agggggatat agtagaggg gagagggctg ttttatacac 60 gtataaatgg tatacaccat ttatacacgg tggtcagaga agctctgatc aggtgacgta120 tgtacagaaa gtcactgtgg cctgagtaga gtcaaggaga aggagcagca agagttgagc180 ttagggaggt ggagaaggg tggaatagat caagcaagac cttggccctg gtagggatct240 gggatttaaa gtgagaggac aaccgttggg atgttgtgag cacagaa 287

- (2) INFORMATION ON SEQ ID NO. 145:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

ggcgacgcct cggtactgac ctctgcagag ccgggtggag cccattgacg tccagcgaac 60 gaggagcagc gatgacggt cgggtgcagc tgataaaggc cctctggcc ttgccgatcc120 ggcctgcgac gcgtcgctgg aggaacccga ttccctttcc cgagacgtt gacggcgata180 ccgaccgact cccggagttc atcgtgcaga cgggctccta catgttcgtg gacgagaaca240 cgttctccag cgacgcctg aaggtgacgt tcctcatcac ccgcctcaca gggcccgcc300 tgcagtgggt gatccctac atcaagaagg agagcccct cctcaatgat taccggggct360 ttctggccga gatgaagcag gtctttggat gggaggagga cgaggacttc taggccggga420 gaccctcggg cctgggggg ggtgctctgg ggagggtccg ctgtgttact ggccgccgcc480 agggtcgca ccggcgccct ccctccgcga gtccctccc ctcgaaaccg ccgcgaagtc540 ccctgcggtg

- (2) INFORMATION ON SEQ ID NO. 146:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1790 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

agtgagaaaq	g cagggactct	teggeetage	g cagccgggac	ccagccagcc	ctgcgcctcg	60
caccatcac	g catgegteet	ggtctttctc	: tagagttgta	ı tatatagaac	atcctggagt	120
ccaccatgaa	cggacagttg	gatctaagto	ggaagctaat	Catcaaaact	caacttgggg	180
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		Ladoararrac	`		
		99999	: LUAGEAAEGA	- France-		
			FEGAFAGEEC	·		300
3-333			LLOTERATION			
	3	ucuauaac	прагадааст	*********		420
	- ccggaacca		Caddaccttc			480
		944444666	CUUCEGAFEC			
aggttatggc	agcaagtatg	tetactttta	atcetttaaa	222222	gaaatcaata	600
aaaatgttat	gtcagcgttt	ggcttaacag	atgatcage	ttas	gaaatcaata cccagtgctc	660
ctqcaqaaqa	tcgttcagga	acaccccaca	acquecayy.	cccagggcca	cccagtgctc gcagctcacc	720
caccaggegt	tcagccacag	Carcaccat	atacage	Clectectca	gcagctcacc	780
ttgaaggtca	gatgtaccaa	Cagtaccac	acacaggage	tcagactcaa	gcagctcacc	840
aggtcccacc	tcagcagcct	Caacagtatg	aacaggeegg	ctatggtgca	cagcagccgc	900
agactggacc	tcaacaacct	Caccacttee	gracicagta	ttcagcaagc	tatagtcagc	960
			accoratates	~~~~~~~		
		34 ccaaccc	aacaacrocc	FACTCRAGGG		~ ~ ~
		4 Cacaacc	auacencea	33Ctta+		
		Caaccccuaa	EGGCTCCAAC	CC33CC+~~~		
			UFACCATOS	~~~*		
	3 - 3		OF CAMMONTS.	# 7 0 0 0 0 0 0 0 b		
,			Udagreada	33222333		
		y	duraraarre	act acons		
J		you addad.	UI AUCAGETE	C++ ~ ~ + + +		
			CLEECTAGCE	T C C C C L C L C L		
		~~~~~~~~	CLUGGGGGGG	アコクセットセッッ ~		
3 3 3		-u-aayatat	Latutataaa	AFGFAAGAGE	~~+~~+~~+3:	740
taataaagat	gattgaatcc	aaaaaaaaa	aaaaaaaaa	aaaaaaaaca	a-caaradari	7 <b>9</b> 0
•	•				· .	1 30

## (2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2357 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ctcgagccga	atcggctcga	gcgcagacct	gcagcgggca	aagagctccc	gaggaagcac	60
agcttgggt	: aggttcttgc	: ctttcttaat	: gttagagaca	gctaccggaa	ggaggggaac	120
aaggagttct	. cttccgcago	: ccctttccc	: acgcccaccc	ccagtctcca	gggacccttg	180
cardaarcat	aggetggaag	, ccatggtccc	: gaagtgtagg	gcaagggtgc	ctcaggacct	240
tttggtcttc	agcctccctc	agcccccagg	atctgggtta	gataaccact	. cctoooteot	300
cctcatggga	agatgtctca	gageetteca	tgacctcccc	teccadece	: aatgccaagt	360
9946669949	, crycacaaag	Leageagga	ccactaaato	: tccaadacct	GG+G+GGGG	420
ggcaggagca	tgtatgtctg	caggtgtctg	acacgcaagt	gtgtgagtgt	gagtgtgaga	480
gatggggcgg	r gggtgtgtct	gtaggtgtct	ctgggcctgt	atataaataa	ggttatgtga	540
gggtatgaag	agctgtcttc	ccctgagagt	ttcctcagaa	cccacagtga	gaccacgcga	600
ctcctggggc	: agagaagttc	cttaggtttt	ctttggaatg	aaattootoo	ttccccccat	660
ctctgagtag	aggaagccca	ccaatctgcc	ctttgcagtg	tacaaaataa	3366t 33636	720
gttggtgtgg	agttggggct	gccatagggt	ctgcagcctg	ctggggctaa	aaggtaagag	
aaggctctgt	cactccagge	atatgtttcc	ccatctctct	ctggggctac	acagtagagg	780
ggcagaagtg	tcaccctgtg	ggtgtctccc	tegggggete	ttcccctaga	cetecenete	840
acttacataa	agctcccttg	aaqcaaqaaa	gagggtccca	agactacaaa	actggaagca	900
cagcctcggg	gatggggagg	gaaagacggt	gctatatcca	gttcctgcta	tctgctcatgl	200
ggtggctgtg	acaaccctgg	cctcacttga	ttcatctctc	gttttcttcc	caccctctgg1	.020
gagtccccat	cccattttca	tectgageee	aaccaggccc	taccattage	ctcttgtcccl	080
ttggcacact	totacccaca	ggtgagggg	aggacctgaa	ggtattggc	tgttcaacaal	140
tcagtcatca	tagatatttt	tgtcaactgc	ttattaatta	atttaggget	gtttgccccgl	200
aatgagaggt	tgaggaaaag	actgtgggtg	gggäggccct	acctggggat	tcccttttcc1	260
tttctggccc	cagoctaggt	ggaggcaagt	ggaatatctt	atattagaga	atttgggggcl	320
teggggagge	agagaatete	ttgggagtct	tagatagaa	taataastta	tgtttcctct1	380
tgatctcaaa	gcacaatgtg	gatttgggga	ccaaacctca	aggigeatte	cccttagagg1	440
acctgagttt	gggagagtgg	tgagtggaag	adaddagcaa	gggacacacc	cctgttttcal	500
ctcagcttaa	ttctccttcc	cagataaggc	aadccadtca	taayaaycay	ctgcaggccc1	560
tecetetact	cttcctatcc	taaaaatagg	aagccatttta	ttacacacac	ccagagagagl	620
gagggactgt	cacactogto	ctgagtgacc	ggaageteet	gaggetetet	tctttaccaal	680
aaccatccat	ccctagaaga	gcacagagcc	Ctgaggggt	gggcgcccgc	gggctgagccl	740
cctggtcttc	tctacagttc	acagaggtet	ttcagctcat	ttaateeeae	gaaagaggcal	800
tcaaagctag	aatgtgaata	taactittot	ggaccaatac	taagaataag	aagaagcccal	860
gtggtgagga	aagtgcgttc	tcccagcact	gcctcctgtt	tteteestet	catgtccctcl	920
cagggaaaat	gactttattg	cttaatttct	acctttccc	catacacaca	gcacttttgg2	980
gcctttttt	atagetggaa	aaaacaaaat	accaccctac	aaacctctat	ttäaaaagaa2	J40
acagaaatga	ccacqtqaaa	tttacctcta	tccaaacatt	teatecatet	gtatgtgtat2	100
gtgtgtgagt	gtgtgaagcc	gccagttcat	Ctttttatat	agaattatt	tctcattttg2	100
gtctgtttta	gtcccctccc	tcatagactt	atactcaca:	ccasagers	aaacgttttg2	220
ggggcttgta	atttatccto	aaaaatttaa	ctttgaggga	aaaaaaaaaa	tgttttaccg2:	280
tgggggggta	aaataaa		gagaga	aaaggggag	cyctctaccg2.	340
,		•			2.	357

#### (2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 907 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

gttcattgtc tggcaccaag ctccttgggg tgaattttct tccaaaagag tccggggagt 60 ccaggtectt ettectggtt acteataacg eggeeceatt teteactece attgggegte120 gggtttctag agaagccaat cagtgtcgcc gcagttccca ggttctaaag tcccacgcac180 eccgegggae teatattttt eccagaegeg gaggttgggg teatggegee ecgaageete240 ctcctgctgc tctcaggggc cctggccctg accgatactt gggcgggtga gtgcggggtc300 cagagagaaa cggcctctgt ggggaggagt gaggggcccg cccggtgggg gcgcaggact360 cagggageeg egeceggagg agggtetgge gggteteage eceteetege ececaggete420 ccactecttg aggtatttca gcaccgctgt gtcgcggccc ggccgcgggg agccccgcta480 categoogtg gagtacgtag acgacacgca attectgegg ttegacageg acgeegegat540 tccgaggatg gagccgcggg agccgtgggt ggagcaagag gggccgcagt attgggagtg600 gaccacaggg tacgccaagg ccaacgcaca gactgaccga gtggccctga ggaacctgct660 ccgccgctac aaccagagcg aggctggtga gtgaacccgg ccgggggcgc aggtcacgag720 cacccccat ccggcacggg accgcccggg tccttcagag ttccgggtgc gaaatgtacc780 ccgagggagg ggaggcgttg gattgctgga gtggatactg ggggggtttt acgcaggttc840 attttcagtt taggccaaaa tccccgcggg ttgggcgggg atggggggg gttaggtggg900 cggggtt 907

- (2) INFORMATION ON SEQ ID NO. 149:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1987 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
aggaggcgtg ggggggggg cgggggagtc agggaagagc accatcgtca agcagatgaa
gatcatccac gaggatggct actccgagga ggaatgccgg cagtaccggg cggttgtcta 120
cagcaacacc atccagtcca tcatggccat tgtcaaagcc atgggcaacc tgcagatcga 180
ctttgccgac ccctccagag cggacgacgc caggcagcta tttgcactgt cctgcaccqc 240
cqaqqaqcaa qqcqtqctcc ctqatqacct qtccqqcqtc atccqqaqqc tctqqqctqa 300
ccatggtgtg caggcctgct ttggccgctc aagggaatac cagctcaacg actcagctgc 360
ctactacctg aacgacctgg agcgtattgc acagagtgac tacatcccca cacagcaaga 420
tgtgctacgg acccgcgtaa agaccacggg gatcgtggag acacacttca ccttcaagga 480
cctacacttc aagatgtttg atgtgggtgg tcagcggtct gagcggaaga agtggatcca 540
ctgctttgag ggcgtcacag ccatcatctt ctgcgtagct tgagcgccta tgacttggtg 600
ctagctgagg acgaggagat gaaccgcatg catgagagca tgaagctatt cgatagcatc 660
tgcaacaaca agtggttcac agacacgtcc atcatcctct tcctcaacaa gaaggacctg 720
tttgaggaga agatcacaca cagtcccctg accatctgct tccctgagta cacaggggcc 780
aacaaatatg atgaggcagc cagctacatc cagagtaagt ttgaggacct gaataagcgc 840
aaagacacca aggagatcta cacgcacttc acgtgcgcca ccgacaccaa gaacgtgcag 900
ttcgtgtttg acgccgtcac cgatgtcatc atcaagaaca acctgaagga ctgcggcctc 960
ttctgagggg cagcggggcc tggcgggatg ggccaccgcc gactttgtac cccccaaccc1020
ctgaggaaga tgggggcaag aagatcacgc tccccgcctg ttcccccgcc gcttttctcc1080
tettteetet etttgttete ageteeeet gteeeeteag etceagaegt aggggagggg1140
ttgccacagg cctccctgtt tgaagcctgc ccttgtctga gatgctggta atggccatgg1200
tacccccttc tgggcatctg ttctggtttt taaccattgt cttgttctgt gatgaggggal260
ggggggcaca tgctgagtct cccaaggctg cgtctggagg ggcccctgct tctccagcct1320
ggacccccag ctttgcccaa caccagcccc tgccccagcc caagtccaaa tgtttacagg1380
gagecteetg cecagteece caaceceage egeteggagg ceceaaagga aaaagcacaa1440
gaagegtgag aegecaceat teetggaaae caeagteeae etgeteatte tegtagettt1500
ttaaaaaaat gaaagtaaag gaaaaaaaaa aaactgcaaa tctagaaaac tttttagaga1560
aaaactattt aaaactgtca gatcctgacc agcaagcgcc cccccagccc cccttccaag1620
tgactccgtg ccttgagtgt gtctgcgtgt ttacacccgt ccctctgctg gccgccccg1680
tgcgagcggc acccctgccc tgccctccac agaattgggt tccaagggct gttccagaca1740
actgccaacg tcactgaggg ccctgccca gcggccctgg ccccaggctc tattaaccta1800
aaatgtaget eeetageget aacetaggaa eegeegetge etgetggggg geeaegeeee1860
tcatgccctt gtcccaggcc cggggccttc agcgttgaac acttccttgc ttttttcaca1920
```

- (2) INFORMATION ON SEQ ID NO. 151:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 2906 base pairs
    - (B) TYPE: Nucleic acid (C) STRAND: individual

      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

gtccagaagc aaaaattaag ttccccaagt tttccatgcc caagatcggc atcccaggtg tgaaaatggg gggtggggga gccgaggtcc atgcccagct accctctctt gaaggagact 120 tgagaggacc agatgttaag ctcgaagggc ccgatgtttc tctaaagggg ccaggagtag 180 acttgccttc agtgaacctc tctatgccaa aagtctctgg gcctgacctt gatctgaact 240 tgaaaggacc aagtttgaag ggagacctgg atgcatctgt teecagcatg aaggtgeatg 300 ctccagggct caacctcagt ggtgtcggtg gcaaaatgca ggtgggagga gacggtgtga 360 aagtgccagg gatcgatgcc acaacaaagc ttaacgttgg ggcaccagat gtgacactga 420 ggggaccaag cctgcaggga gatctggctg tctctggtga catcaaatgc cctaaagtat 480 ccgtaggagc tcctgatcta agcttggagg catccgaagg cagcattaaa cttcccaaaa 540 tgaagetgee ccaatttgge atetetaete eggggteega ettgeaegte aatgeeaagg 600 ggccacaggt ttctggcgaa ctgaaggggc caggtgtgga tgtgaacctg aaagggcctc 660 ggatttcagc accgaatgtg gactttaact tggaaggacc aaaagtgaaa gggagccttg 720 gggccactgg tgagatcaaa ggccccactg tcggaggagg tcttccaggc attggtgttc 780 aaggeetaga aggaaacete cagatgeetg gaattaagte etetggatgt gatgtgaace 840 tgccaggcgt gaatgtgaaa ctcccaactg ggcagatttc tgggcctgaa atcaaaggtg 900 gtctgaaagg ttcagaagta ggtttccatg gggctgctcc tgatatcagt gtgaaggggc 960 ctgcctttaa tatggcatct cctgagtcag attttggcat caacttgaag ggcccaaaaa1020 tcaaaggagg tgcggatgtt tcagggggtg tcagtgcccc agacatcagc cttggtgaag1080 ggcatttgag tgttaaaggt tccgggggtg agtggaaggg accccaagtc tcctctgctc1140 tcaacttgga cacatctaag tttgctgggg gccttcattt ctcaggacca aaggtggaag1200 gaggtgtgaa aggaggtcag attggactcc aggctcctgg gctgagtgtg tctgggcctc1260 aaggtcactt ggaaagtgga tctggaaaag taacattccc taaaatgaag atccccaaat1320 ttaccttctc tggccgtgag ctggttggca gagaaatggg ggtggatgtt cacttccctal380 aagcagagge cagcatecaa getggtgetg gagaeggega gtgggaagag tetgaagtea1440 aactgaaaaa gtccaagatc aaaatgccca agtttaattt ttccaaacct aaagggaaag1500 gtggtgtcac tggctcacca gaagcatcaa tttctgggtc caaaggtgac ctgaaaagtt1560 caaaggccag cctgggctct ctggaaggag aggcagaggc cgaagcctct tcaccgaaag1620 gcaaattctc cttatttaaa agtaagaagc cacggcaccg ctcaaattca ttcagtgatg1680 aaagagagtt ctctggacct tccaccccga cggggacgct ggagtttgaa ggtggggaag1740 tgtctctgga aggtgggaaa gttaaaggga aacacgggaa gctgaaattc ggtacctttg1800 gtggattggg gtcaaagagc aaaggtcatt atgaggtgac tgggagcgat gatgagacag1860 gcaagttaca ggggagtggg gtgtccctgg cctctaagaa gtcccgactg tcctcctctt1920 ctagcaatga cagtgggaat aaggttggca tccagcttcc cgaggtggag ctgtcagttt1980 ccacaaagaa agagtagcag gcctttgtag aacaaaacat cagccttggg tggtgttc2040 ctatataaac tccaaaggga aacacccga ctgcctcagc aatcatgcaa agaccttgcc2100 tggcccggtg gcaagcgctg aaaaaccgac cgcctgtagg ctcctggaac tatacagata2160 ggtaaagagt tocaagttog tocagoocat gtgcaaagtc aacagtattt gcottaagat2220 ttcatatata tatattttt tgcattgact gctgagagct cctgtttact aagcaagctt2280 ttgtgtttat tatcctcatt tttactgaac attgttagtt ttggggtaat ggaaacccac2340 tttttcattg taatgacttt gggggctttt gttagtaagg gtggggggg tgatgggttg2400 cagacggagg tcaggtcttc ctctttcctg agactggatc tgttcaaaca gcaaacgccc2460 acagatggcc cagaggtggt ggtagtcagg gtgtgtgggt gtttttaggg ttctttagtg2520 ttgtttcttt cacccagggg tggtggtccc agccagtttg gtgctgacgg tgagaggaaa2580 ttagaatctg tttgcaaatt gtccaaccca cccctcaac atgaggggct tccattttct2640 gtgttttgta agggaactgt ttccttcatg ccgccatgtt cctgatatta gttctgattt2700 ctttttaaca aatgttatca tgattaagaa aatttccagc actttaatgg ccaattaact2760 gagaatgtaa gaaaattgat gctgtacaag gcaaataaag ctgtttatta accttgaaaa2820 agggaggaa aggggggcgg gggagg. 2906

### (2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2367 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
gesteeeges egeogestet gteteestet etecacaaac tgeeeaggag tgagtagetg
ctttcggtcc gccggacaca ccggacagat agacgtgcgg acggcccacc accccagccc 120
gccaactagt cagcetgege etggegeete eecteteeag gtecateege catgtggeee 180
ctgtggcgcc tcgtgtctct gctggccctg agccaggccc tgccctttga gcagagaggc 240
ttctqqqact tcaccctgga cgatgggcca ttcatgatga acgatgagga aqcttcgggc 300
getgacacet egggegteet ggaceeggae tetgteacac ceaectacag egecatgtgt 360
cetttegget gecaetgeca cetgegggtg gtteagtget eegaeetggg tetgaagtet 420
qtqcccaaaq agatctcccc tgacaccacg ctgctggacc tgcagaacaa cgacatctcc 480
gageteegea aggatgaett caagggtete cageacetet aegeeetegt cetggtgaac 540
aacaagatet ecaagateea tgagaaggee tteageeeae tgeggaaget geagaagete 600
tacateteca agaaccacet ggtggagate eegeecaace tacecagete eetggtggag 660
ctccgcatcc acgacaaccg catccgcaag gtgcccaagg gagtgttcag tgggctccgg 720
aacatgaact gcatcgagat gggcgggaac ccactggaga acagtggctt tgaacctgga 780
geettegatg geetgaaget caactacetg egeateteag aggeeaaget gaetggeate 840
cccaaagacc tccctgagac cctgaatgaa ctccacctag accacaacaa aatccaggcc 900
atcgaactgg aggacctgct tcgctactcc aagctgtaca ggctgggcct aggccacaac 960
cagatcagga tgatcgagaa cgggagcctg agcttcctgc ccaccctccg ggagctccac1020
ttggacaaca acaagttggc cagggtgccc tcagggctcc cagacctcaa gctcctccag1080
gtggtctatc tgcactccaa caacatcacc aaagtgggtg tcaacgactt ctgtcccatg1140
ggcttcgggg tgaagcgggc ctactacaac ggcatcagcc tcttcaacaa ccccgtgccc1200
tactgggagg tgcagccggc cactttccgc tgcgtcactg accgcctggc catccagttt1260
ggcaactaca aaaagtagag gcagctgcag ccaccgcggg gcctcagtgg gggtctctgg1320
ggaacacage cagacateet gatggggagg cagagecagg aagetaagee agggeecage1380
tgcgtccaac ccagccccc acctcgggtc cctgacccca gctcgatgcc ccatcaccgc1440
ctetecetgg cteceaaggg tgeaggtggg cgeaaggeee ggeeeceate acatgtteee1500
ttggcctcag agctgcccct gctctcccac cacagccacc cagaggcacc ccatgaagct1560
tttttctcgt tcactcccaa acccaagtgt ccaaggetcc agtcctagga gaacagtccc1620
tgggtcagca gccaggaggc ggtccataag aatggggaca gtgggctctg ccagggctgc1680
egeacetgic cagacacaca tgttetgite etectectea tgcatticea geetiteaac1740
cctccccgac tctgcggctc ccctcagccc ccttgcaagt tcatggcctg tccctccaag1800
acceptage cartageest tegaceages eterritets theteteth eccepteent1860
tecteagace titetegett etgagettgg tggeetgtte cetecatete teegaacetg1980
gettegeetg tecettteae tecacaceet etggeettet geettgaget gggaetgett2040
tetgtetgte eggeetgeae ecageecetg eccacaaaae eecagggaca geggtetece2100
cagootgooc tgotcaggoo ttgoccocaa acctgtactg toccggagga ggttgggagg2160
tggaggccca gcatcccgcg cagatgacac catcaaccgc cagagtccca gacaccggtt2220
ttcctagaag cccctcaccc ccactggccc actggtggct aggtctcccc ttatccttct2280
ggtccagcgc aaggagggc tgcttctgag gtcggtggct gtctttccat taaagaaaca2340
ccgtgcaacg tgaaaaaaa aaaaaaa
```

## (2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1314 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
cacacacctg cacatactca tgcatgcaca tgtacacacg cagtcacaca tgcactcacg
cagttgcaca cacacgcatg ctcactccca cactgtgtgc actcaggtgg ctgtgttgga 120
cagttgggcc cagggctccc ctgctgtcct gtggggccgg catctgctct ccttctttct 180
coccaggtac ttotactoco gaaggattga catcaccotg togtoagtoa agtgottoca 240
caagetggcc tetgeetatg gggccaggca getgeagggc taetgegeaa geetetttgc 300
catectecte ecceaggace ectegiteea gatgeeetg gacetgiatg ectatgeagt 360
ggccacaggg gacgccctgc tggagaagct ctgcctacag ttcctggcct ggaacttcga 420
ggccttgacg caggccgagg cctggcccag tgtccccaca gacctgctcc aactgctgct 480
gcccaggagc gacctggcgg tgcccagcga gctggcccta ctgaaggccg tggacacctg 540
gagetggggg gagegtgeet eccatgagga ggtggaggge ttggtggaga agateegett 600
ccccatgatg ctccctgagg agctctttga getgcagttc aacctgtccc tgtactggag 660
ccacgaggcc ctgttccaga agaagactct gcaggccctg gaattccaca ctgtgccctt 720
ccagttgctg gcccggtaca aaggcctgaa cctcaccgag gatacctaca agccccggat 780
ttacacctcg cccacctgga gtgcctttgt gacagacagt tcctggagtg cacggaagtc 840
acaactggtc tatcagtcca gacgggggcc tttggtcaaa tattcttctg attacttcca 900
agocccotot gactacagat actacccota coagtootto cagactocac aacaccccag 960
cttcctcttc caggacaaga gggtgtcctg gtccctggtc tacctcccca ccatccaqaq1020
etgetggaac taeggettet cetgeteete ggaegagete eetgteetgg geeteaceaa1080
gtctggcggc tcagatcgca ccattgccta cgaaaacaaa gccctgatgc tctgcgaaqq1140
gctcttcgtg gcagacgtca ccgatttcga gggctggaag gctgcgattc ccagtgccct1200
ggacaccaac agetegaaga gaaceteete etteceetge eeeggeagag etttteaaac1260
gggctttccg caacgggtca atccgcgcct ttctaacttg acaaacttct tcag
```

## (2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 965 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

cctcccaaag gaactcccca atactagaac tcatcccaaa ccccttgcac ttcaacaaat 60 taacgaaccc attececaac ccacaatacc ccacceteca acaacetaaa acaacgaett120 catqctcccg tgcccaaaac gcacagacct tcaacctgga cggctccctg atctatgaaa180 gactcccatc gtcttgcagt cggtcttcac cagcgtgcgg cagaaaatcg agaaggagga240 tgacagtgaa qqcqaggaga gtgaggagga qqaaqaqqqc gaqqaqqaaq qctccqaatc300 cgaatctcgg tccgtcaaag tgaagatcaa gcttggccgg aaggagaagg cacaggaccg360 qctqaaqqqc gqccgqcggc ggccqagccg agggtcccga gccaagccgg tcgtgaqtga420 cgatgacagt gaggaggaac aagaggagga ccgctcagga agtggcagcg aagaagactg480 ageccegaca ttecagtete gacceegage ecetegttee agagetgaga tggcatagge540 cttagcagta acgggtagca gcagatgtag tttcagactt ggagtaaaac tgtataaaca600. aaagaatett eeatatttat acagcagaga agetgtagga etgtttgtga etggeeetgt660 cctggcatca gtagcatctg taacagcatt aactgtctta aagagagaga gagagaattc720 cqaattgggg aacacacgat acctgttttt cttttccgtt gctggcagta ctgttgcgcc780 gcagtttgga gtcactgtag ttaagtgtgg atgcatgtgc gtcaccgtcc actcctccta840 ctgtatttta ttggadaggt cagactcgcc gggggcccgg cgagggtatg tcagtgtcac900 tggatgtcaa acagtaataa attaaaccaa caacaaaacg caaaaaaaaa aaaccaaggg960 cgaga

#### (2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3101 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
ctcgcgccgg acacagggag cagcgagcac gcgtttcccg caacccgata ccatcggaca 60 ggatttctcc gcctcagccc aacgggagg gctagttgca catagtgatt tagatgaaag 120 agctattgaa gctttaaaag aattcaatga agacggtgca ttggcagttc ttcaacagt 180 taaaggacagt gatctctct atgttcagaa caaaagtgcc tttttatgtg gagtcatgaa 240 gacttacagg cagagagaa aacaagggac caaagtagca gattctagta aaggaccaga 300 tgaggcaaaa attaaggcac tcttggaaag aacaggctac acacttgatg tgaccactgg 360 acagagggaag tatggaggac cacctccaga ttccgtttat tcaggtcagc agccttctgt 420 tggcactgag atatttgtg gaaagatccc aagagatcta tttgaggatg aacttgttcc 480 attattgag aaagctggac ctatatgga tcttcgtcta atgatggatc cactcactgg 540 tctcaataga ggttatgcgt ttgtcacttt ttgtacaaaa gaagcagctc aggaggctgt 600 taaactgtat aataatcatg aaattcgttc tggaaaacat attggtgtct gcatctcagt 660 tgccaacaat aggctttttg tgggctctat tcctaagagt aaaaccaagg aacagattct 720
```

tgaagaattt agcaaagtaa cagagggtct tacagacgtc attttatacc accaaccgga 780 tgacaagaaa aaaaacagag gcttttgctt tcttgaatat gaagatcaca aaacagctgc 840 ccaggtaaaa gtgctgtttg tacgcaacct tgccaatact gtaacagaag agattttaga 900 aaaggcattt agtcagtttg ggaaactgga acgagtgaag aagttaaaag attatqcqtt 960 cattcatttt gatgagcgag atggtgctgt caaggctatg gaagaaatga atggcaaaga1020 cttggaggga gaaaatattg aaattgtttt tgccaagcca ccagatcaga aaaggaaaga1080 aagaaaagct cagaggcaag cagcaaaaaa tcaaatgtat gacgattact actattatgg1140 tecaceteat atgececete caacaagagg tegaggegt ggaggtagag gtggttatgg1200 atatoctoca gattattatg gatatgaaga ttattatgat tattatgqtt atgattacca1260 taactatcgt ggtggatatg aagatccata ctatggttat gaagattttc aagttggagc1320 tagaggaagg ggtggtagag gagcaagggg tgctgctcca tccagaggtc gtggggctgc1380 tecteceege ggtagageeg gttatteaca gagaggaggt cetggateag caagaggegt1440 tcgaggtgcg agaggaggtg cccaacaaca aagaggccgc gggcagggaa aaggggtcgal500 ggccggtcct gacctgttac aatgaagact gacttgctat gtgggattac accagaagct1560 tgcagtggag taatggtaag gaaatcaagc aaccttaaat atgtcggctg tataggagca1620 tattctattg cagaagacct tcctatgaag atcatggaat caaatacggg acattgaact1680 aatacttgga ctttgatatg aatttcttta acaattttct ctgcagtgca agttattaaa1740 ctaaagctac tctattttca aaatgtgttc caacagaaat ccttcataac tcctagcatg1800 gtatcttaat aaagaataaa gttcttttaa aaatctgctc taagtagatt tttccccttt1860 tttaaattaa ggatcccaac agtggtattt tgaaatattc tcttgaattt gtgcatttaa1920 attttattgc agtggtatag atgaatgcca ctgatggtat ccttaaattt tatttctqct1980 caccaaggtt aatcatgatt gtctatatct ttttttatagt gatcactttt gaattgtgtt2040 cagatatgca gtttcaggtg taatcatcag agctggttag tcaggcattc cagatagtgg2100 ttcttttcag aaccttttta aaagggttgg ttaactacct cagtagcaga ggattgaact2160 ataccctgtc tgtactgtac atagaaaatc tttgtagata aaagcaaggc ttgttaaata2220 tgatatgagg gtaagatttt aatataccaa atgtaacatt cttagttgcc tttagtttca2280 gaggettgta agaetteete atgaecatea taacaggeet tgettttgte gtattttgtg2340 gctgaaaaag cagccttgct tcttcagata ttgtagttat ttggatgtat aatagtttag2400 caagatgtta cttttgtaag acatcagatg ttcaaaaaag tgcatccgaa cttgtactaa2460 atactgcagt gtccctttat aaaaagtcag actaaaactg acaattgtac agcgaagcct2520 gacattigga tattitgaag tittitcata aatcatagaa attagtatat ggctgtagtt2580 tagcttttta ggtaaaaggt atgtttcatt agtgcatttc ttcctgctga tcactgtaaa2640 catgtgaatc agctttccat ttcttatgca ggtcatgata acttgtagag tagagtacaa2700 tcatttgtgc tatgttttta attttctaaa gcaccttgat gacagtgagt gtccagtggt2760 gaagcatcct ctattgaacc accctcaaaa atttttttgc caagtcctaa gttgatagct2820 ccttccccaa agggatactg cagttatatc acatacccaa taggcaccac gatgaagatc2940 agagettata ettaattaag gttttataea caccagttee eeagtaaatg caaatttaac3000 aagaaaatca gacatgtcat atgttcaaaa tgctcatggc aaacaatcat tttgcattcc3060 tgcaaataaa attgttttat actgtaaaac aaaaaaaaa a

- (2) INFORMATION ON SEQ ID NO. 157:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 983 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

gggcgggag cggcggtcca gactggggag ggacgcgcac cggccaggag gcttcaagag 60 gagggeacta gggecetgeg ageggegtet taaceggegg egetaggaet eegegggaaa120 cggcgggggc ggacgggcgg caccaggacc caggggaacc gcgacgggcg ggcggcgagc180 aggcccggga gccgggaggt gcgggcggcg gcgctggacc cgacgcggcg agagagccc240 cgagatgccg agcaagaaga agaagtacaa cgcgcggttc ccgccggcgc ggatcaagaa300 gatcatgcag acggacgaag agattgggaa ggtggcggcg gcggtgcctg tcatcatctc360 ccgggcgctc gagctcttcc tagagtcgct gttgaagaag gcctgccagg tgacccagtc420 geggaaegga aagaceatga ecacateeca eetgaageag tgeategage tggageagea480 gtttgacttc ttgaaggacc tggtggcatc tgttcccgac atgcaggggg acggggaaga540 caaccacatg gatggggaca agggcgcccg cagggccgga agccaggcag cqqcqqccqq600 aagaacggtg ggatgggaac gaaaagcaag gacaagaagc tgtccgggac agactcggag660 caggaggatg aatctgagga cacagatact gatggggaag aggagacatc acaaccccca720 coccaggoca gocaccocto tgoccacttt cagagoccco cgacaccott cotgocctto780 gestetaste tgestttges escagegess eegggesset cagsacetga tgaagaggac840 gaagaagatt acgactccta gcgccttctg cccccagac catagcccct tttagttggt900 tttagttgct ctggggggag gagagaaggt agagctgttc ttaaatttat taaaaaaaa960 aataaaaggg aaaaaaaaaa aaa

- (2) INFORMATION ON SEQ ID NO. 158:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 293 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

FIDSYRCFQP KQEGAFTCWS AVTGARHLNY GSRLDYTLGD RTLVIDTFQA SFLLPEVMGS 60 DHCPVGAVLS VSSVPAKQCP PLCTRFLPEF AGTQLKILRF LVPLEQSPVL EQSTLQHNNQ120 TRVQTCQNKA QVRSTRPQPS QVGSSRGQKN LKSYFQPSPS CPQASPDIEL PSLPLMSALM180 TPKTPEEKAV AKVVKGQAKT SEAKDEKELR TSFWKSVLAG PLRTPLCGGH REPCVMRTVK240 KPGPNLGRRF YMCARPRGPP TDPSSRCNSS SGAGPAEPME AWGHLAWSPL HMI 293

- (2) INFORMATION ON SEQ ID NO. 159:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ETLREKQEAA QGRGAGLRSC AGVTMPDVPR PPLVQLGLLQ RKNCTGRRGQ WEDPGAWHTC 60 RSGGPSWVLA SSQYASHMAP CGPHRGVCAR APPAQTSRMR SVTPSHLWLL KSWPAPSPLW120 PLPSLLESSG S

- (2) INFORMATION ON SEQ ID NO. 160:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KRRPKLGPGF FTVRITHGSL WPPQRGVRKG PASTDFQNEV RNSFSSLASE VLACPFTTLA60 TAFSSGVFGV MRALISGRLG SSMSGEAWGQ LGEG 94

- (2) INFORMATION ON SEQ ID NO. 161:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

LHQLAAQRLY LRPVRVGAWA LSLPGERRAE ISNQWSALVT WIPEGREGST VSSAADCCSK 60 NVFSTSFESP SHGNPSTPTR DPTPAVSRIS STCTSRDPND SCTNEHYGSC SNCLSTHCVY120 GWKAFGRKKG SSRLKG

- (2) INFORMATION ON SEQ ID NO. 162:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 281 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

PGSQKVAKAV PFPQRRTAAV RMSFPPHLNR PPMGIPALPP GIPPPGFF PPPVPPGTPM 60
IPVPMSIMAP APTVLVPTVS MVGKHLGARK DHPGLKAKEN DENCGPTTTV FVGNISEKAS120
DMLIRQLLAK CGLVLSWKRV QGASGKLQAF GFCEYKEPES TLRALRLHD LQIGEKKLLV180
KVDAKTKAQL DEWKAKKAS NGNARPETVT NDDEEALDEE TKRRDQMIKG AIEVLIREYS240
SELNAPSQES DSHPQEEEG KEGGHFPQIS SGPTDPLSTH H 281

- (2) INFORMATION ON SEQ ID NO. 163:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

CSLVQESLGS LEVQVEEILE TAGVGSLVGV LGFPWEGDSN EVEKTFLLQQ SAAEETVLPS 60 RPSGIQVTSA LHWFEISARR SPGRLSAQAP TRTGRKYSRC AAS 103

- (2) INFORMATION ON SEQ ID NO. 164:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

NISLLDHPGL QSCLYFLFWI LFTNRERYIS AWKWPDVWKL DIWHFGLHSH GYYSHNKDGS 60 GNSFLDLDQP SRYLGIYYIL FCIFLVLWRD SLAIFGLPEY VFCVYSAPVK WFCLVCHNPH120 GCYMSIS

- (2) INFORMATION ON SEQ ID NO. 165:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 382 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

HEVLCCRMAP LQKAKVIRLI KISPEKPITL AVGDGANDVS MIQEAHVGIG IMGKEGRQAA 60 RNSDYAIARF KFLSKLLFVH GHFYYIRIAT LVQYFFYKNV CFITPQFLYQ FYCLFSQQTL120 YDSVYLTLYN ICFTSLPILI YSLLEQHVDP HVLQNKPTLY RDISKNRLLS IKTFLYWTIL180 GFSHAFIFFF GSYLLIGKDT SLLGNGQMFG NWTFGTLVFT VMVITVTIKM ALETHFWTWI240 NHLVTWGSII FYFVFSLFYG GILWPFLGSQ NMYFVFIQLL SSGSAWFAII LMVVTCLFLD300 IKKVFDRHL HPTSTEKAQM YSNTVALSDE FIALQPLSRA RNQLSKLSLL KQMQVSSAWT360 PCAVSRKEKQ RVHLLEECWN EL

- (2) INFORMATION ON SEQ ID NO. 166:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

QELNKHKIHI LGAQKWPENP SIKQGKYKIK YNRSPGNEMV DPSPKMSFQS HLYCDCNNHD60 CEDQSAKCPV SKHLAISKQR CIFPY

- (2) INFORMATION ON SEQ ID NO. 167:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 496 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

RLEKGPLPFQ MPGMRLPETQ VLPGEIDETP LSKPGHDLAS MEDKTEKWSS QPEGPLKLKA 60 SSTDMPSQIS VVNVDQLWED SVLTVKFPKL MVPRFSFPAP SSEDDVFIPT VREVQCPEAN120 IDTALCKESP GLWGASILKA GAGVPGEQPV DLNLPLEAPP ISKVRVHIQG AQVESQEVTI180 HSIVTPEFVD LSVPRTFSTQ IVRESEIPTS EIQTPSYGFS LLKVKIPEPH TQARVYTTMT240 QHSRTQEGTE EAPIQATPGV DSISGDLQPD TGEPFEMISS SVNVLGQQTL TFEVPSGHQL300 ADSCSDEEPA EILEFPPDDS QEATTPLADE GRAPKDKPES KKSGLLWFWL PNIGFSSSVD360 ETGVDSKNDV QRSAPIQTQP EARPEAELPK KQEKAGWFRF PKLGFSSSPT KKSKSTEDGA420 ELEEQKLQEE TITFFDARES FSPEEKEEGE LIGPVGTGLD SRVMVTSAAR TELILPEQDR480 KADDESKGSG LGPNEG

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

SLPASMYWDS KHSHLKFLLA TSLQTAVQMR SQQKFLSFPL MIAKRQPHHW QMKAGLQKTN 60 QKVKNLVCSG FGFQTLGFPL LLMRQVLIPK MTSRDLLPFK HSLRHDQRQN CLKNRRRQAG120 SDFPN 125

- (2) INFORMATION ON SEQ ID NO. 169:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

MGADLWTSFL ESTPVSSTEE ENPMFGSQNQ SRPDFLLSGL SFGALPSSAS GVVASWLSSG 60 GNSRISAGSS SEQLSASWWP EGTSNVSVCC PSTLTLEEII SNGSPVSGWR SPEMESTPGV120 ACMGASSVPS 130

- (2) INFORMATION ON SEQ ID NO. 170:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

VVYRGVKCFI DKKKKTALEP TYSSSSSSS SSSSSSSS SSSSSSSS SSFFFLLFSA 60 LTTPFFAASG FPLARYAAIS FSYFSFTSQP SFHKAACHLQ QCYSTSLPVS SQHHQWTGQD120 VLL

- (2) INFORMATION ON SEQ ID NO. 171:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KKLYLLRSIQ NVNKTAAIFF LQLQSGIQLT EQQLSSYKLH QRQLKMKKIK PKKKTKRKKK 60 KKQKTKLPSP YITNLCCAPT RTCFKFPCQF TTPILYQARL VAIENTTRTG LSKDTFGSVL120 TIQKKTLYSL KTNLTQPYIS IFFFKRSELC TGGLNAL

- (2) INFORMATION ON SEQ ID NO. 172:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 152 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

LNMGKGDPKK PRGKMSSYAF FVQTCREEHK KKHPDASVNF SEFSKKCSER WKTMSAKEKG 60 KFEDMAKADK ARYEREMKTY IPPKGETKKK FKDPNAPKRP PSAFFLFCSE YRPKIKGEHP120 GLSIGDVAKK LGEMWNNTAA DDKQPYEKKA AK

- (2) INFORMATION ON SEQ ID NO. 173:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 281 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

SGSAGPGPRG PRATESGKRM DCPALPPGWK KEEVIRKSGL SAGKSDVYYF SPSGKKFRSK 60
PQLARYLGNT VDLSSFDFRT GKMMPSKLQK NKQRLRNDPL NQNKGKPDLN TTLPIRQTAS120
IFKQPVTKVT NHPSNKVKSD PQRMNEQPRQ LFWEKRLQGL SASDVTEQII KTMELPKGLQ180
GVGPGSNDET LLSAVASALH TSSAPITGQV SAAVEKNPAV WLNTSQPLCK AFIVTDEDIR240
KQEERVQQVR KKLEEALMAD ILSRAADTEE MDIEMDSGDE A

- (2) INFORMATION ON SEQ ID NO. 174:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

IIDIYIKNTS KKALVSAIKK LYVLGYIFFL TGKSQWKHFC SISRNFLLGK VGRKLPDHIL 60 RLHLHCPFOY PSLLYQQLAT RCLPSVLLPI SCVLAVLALP VS 102

- (2) INFORMATION ON SEQ ID NO. 175:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

IYTSKIHLKR HWLVLLKSSM CSGTFFFLQA KASGNIFVQF LGIFSWGKSV ESYLIIFLGF 60

ISTVHFNIHL FCISSSRQDV CHQCFFQFLA YLLYSLFLFP DVFICDNKSF AEGLRCVKPN120 SRVLFHSSGD LPCDWRRACV QSTGNSR 147

- (2) INFORMATION ON SEQ ID NO. 176:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ECPLGARGPW EPRHPFPLGR GARSRHPCTH GRLAPPQSPP HSQQPFHSHC PSRSPQPSLR60 PHPHPLRAQG CNPSLSTTHR WYSWG 85

- (2) INFORMATION ON SEQ ID NO. 177:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

NALWGPGAPG SPATLSHLAG VPAAATPARM AGWHPPRALP TASSLSTVTA LPAVPSLPYG 60 LTRTPSEPRA ATPHYPPRTD GTAGAEQPHV EPERVPGARG QDAGGRMTAC PCLTSWGTTL120 DRGIGQDP

- (2) INFORMATION ON SEQ ID NO. 178:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

MPFGGQGPLG APPPFPTWPG CPQPPPLHAW QAGTPPEPSP QPAAFPQSLP FPQSPAFPTA 60 SPAPPQSPGL QPLIIHHAQM VQLGLNNHMW NQRGSQAPED KTQEAE 106

- (2) INFORMATION ON SEQ ID NO. 179:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 77 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GNPELPWRKF QCQHSCSLWP SPTLWPEIPQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60 LRHMKKLYIN PRQATNP 77

- (2) INFORMATION ON SEQ ID NO. 180:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 64 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

PPTHTRQVGE EIQSCHGENS SVSILAPCGP LLHSGQRYHS QTWSQKGHKG LSTQTAPDPL60 QRLG

- (2) INFORMATION ON SEQ ID NO. 181:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 206 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

RLSCAGTLSG SGPHPSRRLT QGRWVRKSRV AMEKIPVSAF LLLVALSYTL ARDTTVKPGA 60 KKDTKDSRPK LPQTLSRGWG DQLIWTQTYE EALYKSKTSN KPLMIIHHLD ECPHSQALKK120 VFAENKEIQK LAEQFVLLNL VYETTDKHLS PDGQYVPRIM FVDPSLTVRA DITGRYSNRL180 YAYEPADTAL LLDNMKKALK LLKTEL 206

- (2) INFORMATION ON SEQ ID NO. 182:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 206 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RVFQEEELVR RQRNGASGPR PGLRRLRGGR RAVRRKERLL HRQLPAVHKR GARVKLSSPE 60 RDVERDVFLY RAYLAQRKFG VVLDEIKPSS APELQAVRMF ADYLAHESRR DSIVAELDRE120 MSRSVDVTNT TFLLMAASIY LHDQNPDAAL RALHQGDSLE CTAMTVQILL KLDRLDLARK180 ELKRMQDLDE DATLTQLKVL VSLQRV

- (2) INFORMATION ON SEQ ID NO. 183:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 111 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

  LPRPRESEGQ HRGRAGPRDE QERGRDQHHL PAHGRLHLSP RPEPGCRPAC AAPGGQPGVH 60

  SHDSADPAEA GPPGPRPEGA EENAGPGRGC HPHPAQGLGK LATGVKAQGS F 111
  - (2) INFORMATION ON SEQ ID NO. 184:
    - (i) SEQUENCE CHARACTERISTIC:
      - (A) LENGTH: 165 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

GTILPIPEIR RILELLHPLQ AYQDLELGEG GILVQVLHSL QLLPGEVQAV QLQQDLHCHG 60 CALQAVPLVQ RTQGGIRVLV VEIDGGGHEQ EGGVGHVHAP AHLSVQLGHD AVPPTLVGEV120 VSKHAHGLEL RGRGGLDLIQ DHTELPLRQV RSIQEDVPLH VSLWA 165

- (2) INFORMATION ON SEQ ID NO. 185:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

LLSMRMILKP QSFMILMMLR SSNRVTWKLL LIGLDYIRYQ MENQKTSLLL MENSKTRLLL60 LKLLNPLINV GKHCL

- (2) INFORMATION ON SEQ ID NO. 186:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 340 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

RTVIDAMSAL LRLLRTGAPA AACLRLGTSA GTGSRRAMAL YHTEERGQPC SQNYRLFFKN 60 VTGHYISPFH DIPLKVNSKE ENGIPMKKAR NDEYENLFNM IVEIPRWTNA KMEIATKEPM120 NPIKQYVKDG KLRYVANIFP YKGYIWNYGT LPQTWEDPHE KDKSTNCFGD NDPIDVCEIG180 SKILSCGEVI HVKILGILAL IDEGETDWKL IAINANDPEA SKFHDIDDVK KFKPGYLEAT240 LNWFRLYKVP DGKPENQFAF NGEFKNKAFA LEVIKSTHQC WKALLMKKCN GGAINCTNVQ300 ISDSPFRCTQ EEARSLVESV SSSPNKESNE EEQVWHFLGK

- (2) INFORMATION ON SEQ ID NO. 187:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

LSILYILFNG IHWLLGGNLH FSICPPRYFY NHIKQILIFI ISCFLHRNAI FLFRVHLQRN 60 IMKGGNVVTS YILKEEAVIL RAGLAALLSV VQGHSTARPG PCTGPQPQAR SGWGTRAQQP120 QQRAHGVNDG P

- (2) INFORMATION ON SEQ ID NO. 188:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 436 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GRGMGRVQLF EISLSHGRVV YSPGEPLAGT VRVRLGAPLP FRAIRVTCIG SCGVSNKAND 60
TAWVVEEGYF NSSLSLADKG SLPAGEHSFP FQFLLPATAP TSFEGPFGKI VHQVRAAIHT120
PRFSKDHKCS LVFYILSPLN LNSIPDIEQP NVASATKKFS YKLVKTGSVV LTASTDLRGY180
VVGQALQLHA DVENQSGKDT SPVVASLLQK VSYKAKRWIH DVRTIAEVEG AGVKAWRRAQ240
WHEQILVPAL PQSALPGCSL IHIDYYLQVS LKAPEATVTL PVFIGNIAVN HAPVSPRPGL300
GLPPGAPPLV VPSAPPQEEA EAEAAAGGPH FLDPVFLSTK SHSQRQPLLA TLSSVPGAPE360
PCPQDGSPAS HPLHPPLCIS TGATVPYFAE GSGGPVPTTS TLILPPEYSS WGYPYEAPPS420
YEQSCGGVEP SLTPES

- (2) INFORMATION ON SEQ ID NO. 189:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SVLFTGVVSP GPSSLPPPPQ PQGEEGGCRG AGRGWAGPEW ARLGQERRHE ALGAPVPGQR 60 PGLPGEGSTG SALRGQAGFH AAAALLIRRW GLIGVAPRTV LWRKNQGAGS GHWPPGALCK120 VGDSGTC

- (2) INFORMATION ON SEQ ID NO. 190:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 213 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

LVLNVGMQLQ CLPHHIAAEI SAGCEDHAAR LHQLVGELLG GRGHVGLLNV WDAVQVQGAQ 60 DIEHEAALVI LGKPWRVDGG PHLVHDLPER TLKGRGCSGR KQELEGEAVL SSGQAPLVCQ120 RQGTVEVTLL HYPRCVISLV GDPAGTYAGH PDGSERQRCP QAHAHGPSQR LPGAVDDAAV180 AQADLEELHS PHAAASPASR AATPPPAARE SRL 213

- (2) INFORMATION ON SEQ ID NO. 191:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 635 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

GGVSPWRACV QQRMEESEPE RKRARTDEVP AGGSRSEAED EDDEDYVPYV PLRQRRQLLL 60
QKLLQRRKG AAEEEQQDSG SEPRGDEDDI PLGPQSNVSL LDQHQHLKEK AEARKESAKE120
KQLKEEEKIL ESVAEGRALM SVKEMAKGIT YDDPIKTSWT PPRYVLSMSE ERHERVRKKY180
HILVEGDGIP PPIKSFKEMK FPAAILRGLK KKGIHHPTPI QIQGIPTILS GRDMIGIAFT240
GSGKTLVFTL PVIMFCLEQE KRLPFSKREG PYGLIICPSR ELARQTHGIL EYYCRLLQED300
SSPLLRCALC IGGMSVKEQM ETIRHGVHMM VATPGRLMDL LQKKMVSLDI CRYLALDEAD360
RMIDMGFEGD IRTIFSYFKG QRQTLLFSAT MPKKIQNFAK SALVKPVTIN VGRAGAASLD420
VIQEVEYVKE EAKMVYLLEC LQKTPPPVLI FAEKKADVDA IHEYLLLKGV EAVAIHGGKD480
QEERTKAIEA FREGKKDVLV ATDVASKGLD FPAIQHVINY DMPEEIENYV HRIGRTGRSG540
NTGIATTFIN KACDESVLMD LKALLLEAKQ KVPPVLQVLH CGDESMLDIG GERGCAFCGG600
LGHRITDCPK LEAMQTKQVS NIGRKDYLAH SSMDF

- (2) INFORMATION ON SEQ ID NO. 192:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

KPSRRCRPCC RCCIAGMSPC WTLEESAAVP SAGAWVIGSL TAPNSRLCRP SRSATSVART 60
TWPTAPWTSE PTVFPSLQEA SVPKTATSLH IQQPPGQNQH FSSAGLEWAR LVLAACSLCS120
SELLFLFPFT PAAIKAQTSS PKKKKKK

- (2) INFORMATION ON SEQ ID NO. 193:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 150 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

DILLALPECL DGLSPFLLVF APMDGYGLNP LEQQVLVDGV HVCLLLCKDE YRRGCLLQAL 60 EQVHHLGLLL HIFYLLDDIQ AGSPSAPHID GHRLYKGTLS KVLNLLRHGG TEEQGLSLAL120 EVGEDGTDVT LEAHVDHAVS LVQGQVATDV

- (2) INFORMATION ON SEQ ID NO. 194:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 310 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EAPAAARTQS PAAAAQRGDN VYVVTEVLQT QKEVEVTRTH KREGSGRFSL PGATCLQGEG 60 QGHLSQKKTV TIPSGSTLAF RVAQLVIDSD LDVLLFPDKK QRTFQPPATG HKRSTSEGAW120 PQLPSGLSMM RCLHNFLTDG VPAEGAFTED FQGLRAEVET ISKELELLDR ELCQLLLEGL180 EGVLRDQLAL RALEEALEQG QSLGPVEPLD GPAGAVLECL VLSSGMLVPE LAIPVVYLLG240 ALTMLSETQH KLLAEALESQ TLLGPLELVG SLLEQSAPWQ ERRPCPCPPG SWGTAGAKEH300 RPGSCWTSVA

- (2) INFORMATION ON SEQ ID NO. 195:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

TTGIASSGTS IPEDNTRHSR TAPAGPSRGS TGPRLWPCSS ASSKARRASW SRSTPSRPSS 60 SSWHSSLSKS SSSLEMVSTS ARRPWKSSVN APSAGTPSVR KLWRHLIMER PEGSCGQAPS120 LVERLWPVAG GWKVLCFLSG KRRTSKSESI TSWATRNARV LPEGMVTVFF WLRWPWPSPC180 KHVAPGRENR PEPSRLWVRV TSTSFCVCST SVTTYTLSPR CAAAAGLCVL AAAGASHGAE240 244

- (2) INFORMATION ON SEQ ID NO. 196:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 229 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TGHMATGLLA FLGLAAGGQT LCPAGELPGH ARAQASGAPG SVLIAVPGRR RVHTCGPGPA 60
APSTRGECPP PALGHTRPAR PRPVLLRPSC SPGARGAGTW SALLPRGTLL QEAAHQLERP120
QQGLRLQRLR QQLVLRFTQH GQCPQQVDNR DSEFRHQHSG GQHQALQDST CWTVQGLHRP180
KALALLQRLL QGSQGQLVPQ HPLQALQQQL AQLSVQKLQF LGDGLHLCP 229

- (2) INFORMATION ON SEQ ID NO. 197:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TEILPVFVRL AGVPICSTGN ASAMLQPQKP GLSLQQQAEP CLWSGAVHSS VCLVLGLELD60 RGGVSSPSLN SEQTLCLAPV CPGNSPGPHW EPLVF

- (2) INFORMATION ON SEQ ID NO. 198:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AVPRGSLRED GKVRCMSNLL MAGSPLCPLS LALVIAELCA QCCGLAVARL FLWGARAGCG 60 NQSSQTDVSQ AEDSFLAEVS PHLQVSGWGG ARRGRHTPCL T 10.1

- (2) INFORMATION ON SEQ ID NO. 199:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 155 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

VRHTSHLAVL TQGAPGHCSC AAWALLLRTP RAPNEGLGNC LGTLGPGTGS VLNSGKVKRP 60 HLYPAQAQEQ GRQSCGQHPT TDTVLPAAGV RGLVSEAAAW HWHCLCYRWG LLRVSQIQGE120 FQFTQPKGPV CRAALTRAQQ HSTELGKGRG ERVKD 155

- (2) INFORMATION ON SEQ ID NO. 200:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

RMKCSQPPRC HFQSDFQKCA PCPRAQTHWL EPPGRVQTIS SMRNAQKGFA DSIRLWRLPA 60 SGVGWVVSPP IQTQEVAPEG MYLVGSSSGT LGGCRALTQV FLSLSSLGCV CACACACLCF120 SLWAHQDAPR RACARVPT 138

- (2) INFORMATION ON SEQ ID NO. 201:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

VHGREARLGT LAGTAALKPA LLSGYQTFKG QDVLRRVPVA ARRPAGACPR VTAWRCWGSG 60 HLPCLECQEG EAFEEASVLA ARSLSQPLPG SCTGQGLIPC HAGPLEQVGW GWYVLSPQPW120 QPCPLGKVIS DL

- (2) INFORMATION ON SEQ ID NO. 202:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

RLFIGCSLQN KQRWDWGPSL GPCTPLSRAY NHVHRPGRGP ALCPTKSSLH QSSWSPPLRD 60 PAQLPRSWGI GTRVPWRVQE MRRIPCTLRR TPTPELWSRG HCERRQRERH VEDTLTDPVG120 SGRAEDRHTK P

- (2) INFORMATION ON SEQ ID NO. 203:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 76 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

  LAAIKDQLEG VQQALSQAAP IPEEDTDTEE GDDFELLDQS ELDQIESELG LTQDQEAEAQ60
  QNKKSSGFLS NLLGGH
  - (2) INFORMATION ON SEQ ID NO. 204:
    - (i) SEQUENCE CHARACTERISTIC:
      - (A) LENGTH: 102 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

RVCSKHFLRL PPSQKRTQTL KKVMTLNYLT SQSWIKLRVN WDLHKTRKQK HSKIRSLQVS 60 FQICWEAINL GISLQQSTKN TKKISNKKKK KKRKRKKLNC KL 102

- (2) INFORMATION ON SEQ ID NO. 205:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ICLHHNHCLC DTQLLAFYGL IPPTARLEMA VNGACFFTNK PKSTTAEITW KRFSLSRVLK60 YTFKFFPKKL ILIVFPKSFN 80

- (2) INFORMATION ON SEQ ID NO. 206:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 76 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

GKPAALEAHQ GSRLQGRSRE QAAIPPLLSS RTQLCGLGFL FAGLAPCRTL VLELEGPILP60 RGDSQGCRGI GWRRVL 76

- (2) INFORMATION ON SEQ ID NO. 207:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 72 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

NLRVSQLPWK PTRAPDCREE AGSRQPYLHS CPQGLSCVAL DFFLRDLRPA GHWCWSWRVL60 SCPGVTPRVA GG

- (2) INFORMATION ON SEQ ID NO. 208:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

  PGMSSLQDRH GRTIWFQVGP YCSHRQRPQE ADGWKRGVTI TGVVMLRVCL DPPRTTLFLR60

  VTPLPSHASQ GCS

  73
- (2) INFORMATION ON SEQ ID NO. 209:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

QRWLWTSSTS PCWIRAFLPP AGQVWPCSLG RAPAPLTTLQ LTMQLMPKLW CPVCSSPGSH 60 CHLQRGSLLR PTLLHLAPPW LLAWPNLAFC AMLELELLLF FRGGNRVESG KGLAPKCCCC120 GFFAFSKDAL PGPKLQTAVL SKQVRSLGFG AHLLSGSISI LLLATSGQRP PQPHIARCWQ180 KG

- (2) INFORMATION ON SEQ ID NO. 210:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

VGPGKQPWWG QVKQCGSQQG TPLKVAVAPR AAAHWTPQLW HQLHGELQSG QRGWGPAKRA 60 RPDLPSGRQE GPDPARRSRG SPQPPLLLIA TGTSGDRLCS WESRSPGFVG LPAGDRHVSH120 RERPGSRPQL 130

### (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VTGKGRDPGL SCSSSWKRWS RTVTIHADTE QQYETEQLRA VSSSAEAAWA ATPPFCNHPM 60 MSPPHLTSRW GWMAEQMKPA LWRGSLTEMH TFMGEVDGHL TSLMFHTVDC T 111

- (2) INFORMATION ON SEQ ID NO. 212:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 243 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

DVQVAGPEPD CRVHSHVLPG QAHRLAPGPY SVGESLQPRE GCEDCDRQKA NLRIRFKPSL 60 FQHVGTHSSL AGKIQKLKDK DFGKQALRKE HVNPPAEVST SLKTYQHFTL EKAYLREDFF120 WAFTPAAGDF IRFRFFQPLR LERFFFRSGN IEHPEDKLFN TSVEVLPFDN PQSDKEALQE180 GRTATLRYPR SPDGYLQIGS FYKGVAEGEV DPAFGPLEAL RLSIQTDSPV WVILSEIFLK240 KAD

- (2) INFORMATION ON SEQ ID NO. 213:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

GRTGVSVVMG IPSVRREVHS YLTDTLHSLI SELSPQEKED SVIVVLIAET DSQYTSAVTE 60
NIKALFPTEI HSGLLEVISP SPHFYPDFSR LRESFGDPKE RVRWRTKQNL DYCFLMMYAQ120
SKGIYYVQLE DDIVAKPNYL STMKNFALQQ PSEDWMILEF SQLGFIGKMF KSLDLSLIVE180
FILMFYRDKP IDWLLDHILW VKVCNPEKDA KTVTGRKPTC GSASNRPSSS TWALTPRWLA240
RSRN

- (2) INFORMATION ON SEQ ID NO. 214:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 210 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

PAESQPADPL QTVPLPARGH SLLAGWQDPE TEGQRLWKAG AAEGACEPAS RGEHEPEDIP 60 ALHPGESLPA RGLLLGLHPC RGGLHPLPLL PTSKTGAVLL PQWEHRAPGG QALQHVCGGA120 ALRQPSVRQG GPAGGPHRHP PVPSEPRRLP PDRLLLQGSG RGRGGPSLRP SGSTAPLDPD180 GLPCVGDSER DLPEKGRLSC GLLRVPCGQP 210

- (2) INFORMATION ON SEQ ID NO. 215:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAGLVHGSA DWPCLAPWRV SSCFLPGTEL RGLGAPGAKS RLWCRGGGLS LNRHPEVLLR 60 CWVHPEWHGE QLWPVLLPRP VLGKLSSGPS LQRPRMGWVW GTHGEWPEEL RVKRAPVCWL120 QRPGAPLS

- (2) INFORMATION ON SEQ ID NO. 216:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FPQDWPRKEH RPQLLPVPLR VDPASQEHLR VSVKRQASTP APEPALSSRC PQTPQLCARQ 60 EAARHTPGRQ ARPVRGPMDK PSPASGKTGP FPTGHAPELW QIAGAIVWGE FNKSPFENEK120 KKKK

- (2) INFORMATION ON SEQ ID NO. 217:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

VPHTHPILGL CKEGPELSFP RTGLGRSTGH SCSPCHSGWT QHLRSTSGCR LRDRPPPLHQ 60 SLLLAPGAPR PRSSVPGKKQ LDTRQGAKHG QSADPWTSPA PPQGKQGLSL QDTPQSCGRL120 QEPSCGENLI KALLKMKKKK KK

- (2) INFORMATION ON SEQ ID NO. 218:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 379 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

RRGLEGFNGG WTEMPGILWM EPTQPPDFAL AYRPSFPEDR EPQIPYPEPT WPPPLSAPRV 60
PYHSSVLSVT RPVVVSATHP TLPSAHQPPV IPATHPALSR DHQIPVIAAN YPDLPSAYQP120
GILSVSHSAQ PPAHQPPMIS TKYPELFPAH QSPMFPDTRV AGTQTTTHLP GIPPNHAPLV180
TTLGAQRPPQ APDALVLRTQ ATQLPIIPTA QPSLTTTSRS PVSPAHQISV PAATQPAALP240
TLLPSQSPTN QTSPISPTHP HSKAPQIPRE DGPSPKLALW LPSPAPTAAP TALGEAGLAE300
HSQRDDRWLL VALLVPTCVF LVVLLALGIV YCTRCGPHAP NKRITDCYRW VIHAGSKSPT360
EPMPPRGSLT GVQTCRTSV

- (2) INFORMATION ON SEQ ID NO. 219:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

VDTDECQIAG VCQQMCVNYV GGFECYCSEG HELEADGISC SPAGAMGAQG SQDLGDELLD 60 DGEDEEDEDE AWKASTVAGR RCLGSCGWSL RSRLTLPWPI DRASQRTESH RYPTRSPPGH120 PRSVPPGSPT TPQCSPSPGL WWSLPRIPHC LLPTSLL 157

- (2) INFORMATION ON SEQ ID NO. 220:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 211 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

PPPPGPLCLL PIKSLCLLPP SPQPSPPSCP LRAPLTRPHP SALHIPIPKP PKSQGKMAPV 60
PSWPCGCPHQ LPQQPQQPWG RLVLPSTARG MTGGCWWHSW CQRVSFWWSC LHWASCTAPA120
VAPMHPTSAS LTAIAGSSML GARAQQNPCP PGAASQGCRP AEPACDGVQT PLMEYGALDT180
WPGLHQGPMG AAQLDRWLPA PQAQPGSSLN H

- (2) INFORMATION ON SEQ ID NO. 221:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

LGEPQISGAQ PGRVWGQLCQ STSQAHPLPG MPWDHGQGRL WGSETPLLST PSQNTLRVSG 60 LWREWGGRKN WHLPREGDER FALILREASE KCFKCVCMRQ AVGSGGLSSP LPPSFPK 117

- (2) INFORMATION ON SEQ ID NO. 222:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 198 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

NKELSSLKSS DVVMTHTESC ITVASRATHL FGLSDGHSFT TQQQTPHTGT RMSASTWEAV 60 AEPGRWPGPD HGLSGAGHQG VRVPMLPQGV GMTGRSLVTR QWTSLGEGWR ERAGQAPAAH120 RLAHANTLKA LLGGFSENQG EALVSFPRKV PILPPAPLSP EPRDPQGVLA GGAKQRCLRP180 PEPSLPMIPR HARQGVGL

- (2) INFORMATION ON SEQ ID NO. 223:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

SHGMPGRGWA CEVDWHSCPH TLPGWAPEIW GSPSQHGVLG ACPGPFTRTE APHPLSHFSR60 WKTQRRKRPW GGVPSCLQLA PWVPLCGGSP DSISSASE 98

- (2) INFORMATION ON SEQ ID NO. 224:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 298 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATRRRAAEAG MAAVLQRVER LSNRVVRVLG CNPGPMTLQG TNTYLVGTGP RRILIDTGEP 60
AIPEYISCLK QALTEFNTAI QEIVVTHWHR DHSGGIGDIC KSINNDTTYC IKKLPRNPQR120
EEIIGNGEQQ YVYLKDGDVI KTEGATLRVL YTPGHTDDHM ALLLEEENAI FSGDCILGEG180
TTVFEDLYDY MNSLKELLKI KADIIYPGHG PVIHNAEAKI QQYISHRNIR EQQILTLFRE240
NFEKSFTVME LVKIIYKNTP ENLHEMAKHN LLLHLKKLEK EGKIFSNTDP DKKWKAHL 298

- (2) INFORMATION ON SEQ ID NO. 225:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 58 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GFSWGRSPLG RCWCLGGSWD PGYSPTHARL DWTAARRAAV QQPFPPQPPA GVSPIWIL 58

- (2) INFORMATION ON SEQ ID NO. 226:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

SGSLSLNHIS IFQINILLLS ISYNFFSLRI PWEFFNAIGS VIIDAFTNIS YASRMISVPV60 SHYNFLDCCV KFS 73

- (2) INFORMATION ON SEQ ID NO. 227:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 141 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AFLLRPSVTA STRLLPVCAS PRSSPGPSPA QQQQAWQQAW SSARAPSRCR ARPSSSERPC 60 PAVGRLASLY CCCMVFASPP RPGRTWVHCT GWPRLATGLW PLTCQVWGTP RKQQPLPLLG120 SWPLAASWRL WWMPWSWAPR L

- (2) INFORMATION ON SEQ ID NO. 228:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

VPPPALGHRQ HAPASRLRES TQLPRPFTST AAAGMAASVE QREGTIQVQG QALFFREALP 60 GSGQARFSVL LLHGIRFSSE TWQNLGTLHR LAQAGYRAVA IDLPGLGHSK EAAAPAPIGE120 LAPGSFLAAV VDALELGPPV VISPSLSGMY SLPFLTAPGS QLPGFVPVAP ICTDKINAAN180 YASVKTPALI VYGDQDPMGQ TSFEHLKQLP NHRVLIMKGA GHPCYLDKPE EWHTGLLDFL240 QGLQ 244

(2) INFORMATION ON SEQ ID NO. 2:	(2)	229
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- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

WTDHNRGAQL QGIHHSRQEA ARGQLPNRGR GCCFLGVPQT WQVNGHSPVA SLGQPVQCTQ 60 VLPGLGGEAN TMQQQYREAS LPTAGQGLSE EEGLALHLDG ALALLHACCH ACCCCAGEGP120 GELRGLAQTG SRRVLAVTEG RRRN

### (2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

LEFFIPCLGS VNEACLFPGV SFHGLYFSSS SGSFAGSSLW KLHERWLGLG FAGVYSRVKA 60 EWDLRPRLGT TQAEKGRFHH SQCPPHSTTS ARAPPSLLPH PAIVRGATVG RRVPRRGLFL120 135 LPVPEKAFPL LKFKH

## (2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids

  - (B) TYPE: Protein(C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GGPVCWEPQV TPFSSYSVPG ASCPPLQILG KENVYVAGYC MVTSEGRPLG THLPTAAQAR60 AQAHLLVLRP QIKPSPHHMA SDRFLPSRKF CGCAVL

- (2) INFORMATION ON SEQ ID NO. 232:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 83 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CCGEGTVNDG NVPSQPGSCL TWVSNPTLPS PWSTLQRSRG PANAREVSTE KSLQNSHWKR60 RNKGHGKKPQ GRDRPRSQTL GRE

- (2) INFORMATION ON SEQ ID NO. 233:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 52 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

- (2) INFORMATION ON SEQ ID NO. 234:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

LGSAWQQLRR PEASETLRLV GTHRPRQRAL PRQRVASPPP RRGLGLTSPP VRLGQVVPGL60 MPGVVSAAGT QVRRLDEVPA SLRLQHHLQL REGL 94

- (2) INFORMATION ON SEQ ID NO. 235:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

ARPSRSWRWC CSRSDAGTSS RRRTWVPAAL TTPGIRPGTT CPRRTGGEVR PSPRRGGGLA60 TRCLGKARWR GLCVPTSRRV SDASGRRSCC QAEPR 95

- (2) INFORMATION ON SEQ ID NO. 236:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 174 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

APTNTRSSSK FATSGSPGYP IASSGASPEV RQRRTTFFRF RPGESLCGDM KLLTHNLLSS 60 HVRGVGSRGF PLRLQATEVR ICPVEFNPNF VARMIPKVEW SAFLEAADNL RLIQVPKGPV120 EGYEENEEFL RTMHHLLLEV EVIEGTLQCP ESGRMFPISR GIPNMLLSEE ETES 174

- (2) INFORMATION ON SEQ ID NO. 237:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 225 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

YRAQKHCVWC HWVKGWGYTR QNSETGYRST KIHSHNKKNW RLAQSTLSFL FTQQHVGDPA 60
ADGEHTSRFR ALQGALYHFH LQQQVVHGPQ KLLILLISLN RPFRHLDQTQ VIGRLQERRP120
LHFRYHTRHE VGVEFHRADT DLGGLEAQGE ATGPHPPHMR AQQIVGKQFH VAAQTLARPE180
PEKGRPPLPH FRGCSTRCYW IARRTGSGEL AGTSRVCGSS FLYAN 225

- (2) INFORMATION ON SEQ ID NO. 238:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 209 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TFNEKKIYNT ELKNTVFGVI GSRVGDTHGR IRKQGIDQQK YTVITRKTGA WHNQLSVSSS 60 LSSMLGIPRL MGNIRPDSGH CRVPSITSTS SSRWCMVLRN SSFSSYPSTG PFGTWIRRKL120 SAASRNADHS TLGIIRATKL GLNSTGQIRT SVAWRRRGKP RDPTPRTCEL SRLWVSSFMS180 PHKLSPGRNR KKVVLRCLTS GDAPLDAIG 209

- (2) INFORMATION ON SEQ ID NO. 239:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIIKVFSE SVGVSVNGCA LGGTVERCAK 60 SELQTIGQGH GVATRRLSA GAPPRTHSQQ SSHWEELKNK HLQGRGKRPR SRRSRARASA120 ARGAPTGSQR GGSPKRARSG RSRVLA 146

- (2) INFORMATION ON SEQ ID NO. 240:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 134 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

SRTFSFLSFL HCANILTLFV SFQEPHRHIQ VKRSLNKCLQ PSQCKNKYQS SRRSSSRAAP 60 KVPTATPNNY KSVQRECWRE CEWVCAGGHG GAVCKIGVAN HRTRAWSGYP PPTQRGRASP120 HTLTAEFALG RVKK

- (2) INFORMATION ON SEQ ID NO. 241:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

PARTRORPLL ARFGLPPRCE PVGAPLAALA LARERRERGR FPRPCKCLFF NSSQCELCCE 60 CVRGGAPALS RRRVATPCPC PMVCNSDFAH RSTVPPSAHP FTLTPTLSLN TFIIVRRGRW120 DFGRSAAATA SGGLIFIFAL RWLKAFI 147

- (2) INFORMATION ON SEQ ID NO. 242:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PVLCRGNSGS LSRKFPPKPQ KPADKDHPRT CVYLENRSPG KSDLSATPGR SGLESGYQNL60 LRQHQPHGRC PTWPGSRWKV PRRFPGYG 88

- (2) INFORMATION ON SEQ ID NO. 243:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

QDGCPDSGDF AALQSLLKAS SKDVVRQLCQ ESFSSSALGL KKLLDVTCSS LSVTQEEAEE 60° LLQALHRLTR LVAFRDLSSA EAILALFPEN FHQNLKNLLT KIILEHVSTW RTEAQANQIS120 LPRLVDLDWR VDIKTSSDSI SRMAVAPPGL VPDGRFQGGS QAMG 164

- (2) INFORMATION ON SEQ ID NO. 244:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 87 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

FAWASVLQVD TCSRMIFVSR FLRFWWKFSG KRARIASAED RSRNATSLVR RCRAWSSSSA60 SSWVTDKLEH VTSKSFFKPR AELEKLS 87

- (2) INFORMATION ON SEQ ID NO. 245:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 129 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear.
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

DGPGGPTAHP HRCAHPPGVC PGQAPAHLLL CAAAPGHPGQ GQQPAAGGLV GDADRAGDLE 60 CSPRRIFLHP RLHPPRHLGS CHLDRGCGCA GWSCCLHLRE TGWYILGPAE DSASAGSFLH120 SHRCPQTLE 129

- (2) INFORMATION ON SEQ ID NO. 246:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 268 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

ASPSNSQPTS PASAPALPPP ARRSRGAQTV SLTMGTADSD EMAPEAPQHT HIDVHIHQES 60
ALAKLLLTCC SALRPRATQA RGSSRLLVAS WVMQIVLGIL SAVLGGFFYI RDYTLLVTSG120
AAIWTGAVAV LAGAAAFIYE KRGGTYWALL RTLLALAAFS TAIAALKLWN EDFRYGYSYY180
NSACRISSSS DWNTPAPTQS PEEVRRLHLC TSFMDMLKAL FRTLQAMLLG VWILLLLASL240
APLWLYCWRM FPTKGKRDQK EMLEVSGI 268

- (2) INFORMATION ON SEQ ID NO. 247:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

DCTQDPQHDL HHPRGHQQPA AAPGLGGPGP QRRAAGEQEL GQGRLLVDVH IDVGVLWGLR 60°GHLITVGCSH CQGHSLRSSG PASGRREGWG AGWRSGLRVG GGG 103

- (2) INFORMATION ON SEQ ID NO. 248:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

GSRRRDGGGA GAAPVAPRAL GRRARAGRCS EDEGGGGAQR VWGEQPVLAS GQSPPGQEGS60 FTRVWTRASL PTLGQVLQPG GVHVQV

- (2) INFORMATION ON SEQ ID NO. 249:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 154 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

ARGGAMAAGL ARLLLLIGLS AGGPAPAGAA KMKVVEEPNA FGVNNPFLPQ ASRLQAKRDP 60 SPVSGPVHLF RLSGKCFSLV ESTYKYEFCP FHNVTQHEQT FRWNAYSGIL GIWHEWEIAN120 NTFTGMWMRD GDDCRSRSRQ SKVELACASP SNCV

- (2) INFORMATION ON SEQ ID NO. 250:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

PLDAVARART RQLHLALPAP GTAVVTVPHP HAREGVVGDL PLVPDAEDPT VGVPAEGLLV60 LGHVVERAEL ILVRGLHQAE ALARESEEMH GSRHG 95

- (2) INFORMATION ON SEQ ID NO. 251:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 240 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

KVTDGHTRTP RSGVPRQHEA GSPGLTASHA MSIHLAGSLT AMDSICASER SQGVWRAPTP 60 GCQGLSPGPR PGELPGGSSP EERLGRLAVA GPPRGAQNVS QAGPEAEAPP LRFGHAWGAQ120 TPRLGAPGPW TPLPTLPSHI PPFWSQTPAQ RKEGFTEEGQ GRAWPQGGDE DISGPGSCRL180 LWEEEPCVCK LLGLAARPTA GPSLDPCTWP SSCPLAAPGL GTGIEPRGLG WLGQGRDREG240

- (2) INFORMATION ON SEQ ID NO. 252:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 216 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSQRKARA EPGPREGMRT 60 FPVQVAAGCS GRKSHASVNC WGWRPAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120 WARAGTGRGS TSDPDVGWLC PPRREAQQTS YTKAKSTIGE PRSHFMGRRP RPQGPQSKAR180 GRFIPEDSPP GAAPAWGGVS RPLGCLSVCG TPWSTP 216

- (2) INFORMATION ON SEQ ID NO. 253:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 218 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

VLRRLYIYIL YITNMKWFST QPLWLNTKQR SHRRGPGPPP APLSGVLGSR GLPHHPSQGW 60 GRAGPRAGAN VAWNSNCIVR WVGGQWARGC SQPGPFTTNL AMTCGGPWGS GCLLGSTLSE120 VSPWAPPSCP QGHPVLPTRL WAWGLQDPLC RVRVGAGHGS RHQPDAPVGV ARSWDGVVRN180 TAPKTQNKNT TNGRRSPPPT EVGFEPLLIF PVSFLQPW 218

- (2) INFORMATION ON SEQ ID NO. 254:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

RDGGGAGAAP VAPRALGRRA RAGRCSEDEG GGGAQRVWVS SLAGWRLERG TARARSPLTL60 PLPVGGTTRS CLRPVASRP 79

- (2) INFORMATION ON SEQ ID NO. 255:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(Xi)	SEQUENCE	DESCRIPTION	ON: SEQ II	NO: 255:	
		KVSGERARAV	PRSSRQPARL	LTQTRWAPPP	PSSSLHLPAR60
ARRPRARGAT	GAAPAPPPS				79

- (2) INFORMATION ON SEQ ID NO. 256:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

WPGGDWPEAR TGCSTYGKRQ GQRGTGPGRP PLEPPAREAA HPNALGSSTT FIFAAPAGAG60 PPAESPRSNR SRASPAAIA

- (2) INFORMATION ON SEQ ID NO. 257:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 51 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - ORIGIN (vi)
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GHLGGPTGSV CSRILLASSP FYMNCCINKH RVPETTEVII LPTECWPGQA W

- (2) INFORMATION ON SEQ ID NO. 258:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 49 amino acids
    - (B) TYPE: Protein

(2)

(2)

(vi)

ORIGIN

(A) ORGANISM: HUMAN

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: ORF	•
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:	
GGGFLGQIDK SKDNISLVTV IQLHSYTVAL FGLSHEEVLV TNYVFVGCF	49
) INFORMATION ON SEQ ID NO. 259:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 48 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:	
AFTRNTTNKV SDMLANQARL RSLRRPNWLC LLKDSSGLVS ILHELLHK	48
) INFORMATION ON SEQ ID NO. 260:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 179 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	•

PGISVSVDKM ESSPFNRRQW TSLSLRVTAK ELSLVNKNKS SAIVEIFSKY QKAAEETNME 60 KKRSNTENLS QHFRKGTLTV LKKKWENPGL GAESHTDSLR NSSTEIRHRA DHPPAEVTSH120 AASGAKADQE EQIHPRSRLR SPPEALVQGR YPHIKDGEDL KDHSTESKKM ENCLGESRH 179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

(2)	INFORMATION	ON	SEQ	ID	NO.	261:
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- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

QATLLLEPKL TKKNKSTPDL DSGHLLKPSF RVDIPTSRTV RILKTTQQKV KKWKIV 56

- (2) INFORMATION ON SEQ ID NO. 262:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

DSAPSPGFSH FFFNTVRVPF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLLT60 RESSLAVTLN DSEVHCRLLN GDDSILSTDT EIPG 94

- (2) INFORMATION ON SEQ ID NO. 263:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

VMSDPADKAA RADSARAARG KRKKNVEENM AYSALMEVAG YCLIERMLWN PMLKIKSVWL60 CSYAVMVIPR QLAKV

- (2) INFORMATION ON SEQ ID NO. 264:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 74 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AMFSSTFFFL LPRAARAESA RAALSAGSLI TYAFYKRLPK KKLLTRNVDK PLKANKQQTV60 VFAFSYSWQA EVRA

- (2) INFORMATION ON SEQ ID NO. 265:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 63 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

DSKAFSLLSS NQPLPSKLSR PCFPPHFFFF YLEPLEPNRL EPPCLLDHSS PTHFIKGYPK60 RNC

- (2) INFORMATION ON SEQ ID NO. 266:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

RRGSGSRSSM APVLASMLWM STRGTAMTST SLCTSRARSR PMPSSSSPTP TAWRCCCATR60 TRVSTSTRTG ASLRMWCCSG GRCLLLWPTS APTR 94

- (2) INFORMATION ON SEQ ID NO. 267:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 254 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GDRKPLYHYG RGMNPADKPA WAREVKERTR MNKQQNSPLA KSKPGSTGPE PPSPQASPGP 60
PGLPWAPKPY HKFMAFKSFA DLPHRPLLVD LTVEEGQRLK VIYGSSAGFH AVDVDSGNSY120
DIYIPVHIQS QITPHAIIFL PNTDGMEMLL CYEDEGVYVN TYGRIIKDVV LQWGEMPTSV180
AYICSNQIMG WGEKAIEIRS VETGHLDGVF MHKRAQRLKF LCERNDKVFF ASVRSGGSSQ240
VYFMTLNRNC IMNW

- (2) INFORMATION ON SEQ ID NO. 268:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 231 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GKKHLVIPLT QELEPLSSFV HEDPVEVARL HRADLNGFLT PAHYLVGADV GHRSRHLPPL 60 QHHILNDAPV RVDVDTLVLV AQQHLHAVGV GEEDDGMGRD LALDVHRDVD VIAVPRVDIH120 SMEASTGAID DLEPLPLLYC QVDQQRAVGE VGKGLEGHEF VVGFGGPGEA WGPWGGLGAG180 GLRPRAAWLA LGQGRVLLLV HPCSLFYLSG PGWFVSGIHA PTIMVQGLPV P 231

- (2) INFORMATION ON SEQ ID NO. 269:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 454 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GAGCTSPGLW ARKAAARCLP TYPSRAQPSN VGRRRRRPG LGALAAGVPA MAESVERLQQ 60 RVQELERELA QERSLQVPRS GDGGGGRVRI EKMSSEVVDS NPYSRLMALK RMGIVSDYEK120 IRTFAVAIVG VGGVGSVTAE MLTRCGIGKL LLFDYDKVEL ANMNRLFFQP HQAGLSKVQA180 AEHTLRNINP DVLFEVHNYN ITTVENFQHF MDRISNGGLE EGKPVDLVLS CVDNFEARMT240 INTACNELGQ TWMESGVSEN AVSGHIQLII PGESACFACA PPLVVAANID EKTLKREGVC300 AASLPTTMGV VAGILVQNVL KFLLNFGTVS FYLGYNAMQD FFPTMSMKPN PQCDDRNCRK360 QQEEYKKKVA ALPKQEVIQE EEEIIHEDNE WGIELVSEVS EEELKNFSGP VPDLPEGITV420 AYTIPKKQED SVTELTVEDS GESLEDLMAK MKNM

- (2) INFORMATION ON SEQ ID NO. 270:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

KLTVPKFNRN FNTFCTKIPA TTPIVVGRLA AQTPSRFRVF SSIFAATTSG GAHAKQADSP 60 GIISCICPET AFSLTPDSIH VCPSSLQAVF IVIRASKLST QLRTRSTGFP SSNPPLLILS120 MKC

- (2) INFORMATION ON SEQ ID NO. 271:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 176 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

CSSEYVLLE LYLILLDEVG RKVYSYWLVP PCHNQRVATY QCHILSAFQQ SHYLLHQHLL 60 LLRQRYGFSH SRLQFPFVSM PSSGCRDSNP PPLSSSSRCG PGRPLRRRSS GPADSSPGQV120 PAPAPGPAAA GAPQTPPWLG LRPPTLPARA FAAAFAPRCS AGPARGTWGG TSPLPS 176

- (2) INFORMATION ON SEQ ID NO. 272:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

EARQAWTGAK GAGSLTFSSL QSGHLASGSQ SPESTKAPGT PPTPSYPGTP SRQLLWQWVQ 60 PRPALPASSP CSRHQLYLPR QAMSWLLSPA PSVPLDFSGA SPVWATLCFP HPRLPHR 117

- (2) INFORMATION ON SEQ ID NO. 273:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

APALPPPAGN VLASQPSTIC SPRLLRGQPS LGHPLFPSSS APTQVTDPAD SFSLGKVGCC60 LTSPSSPPPI HTHRHPPTPG RLVSHM 86

- (2) INFORMATION ON SEQ ID NO. 274:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 177 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

EARTLPAGGG RAGAYCRERR LAVLAWAGPT AITVAYLGSL GRMEWVGCQG LWCFLVIGTL 60 MPSAHFAKKK KLMTLLPWLL SMLAWPPRVG GTSPLLAEAG EQVLSYDPIH QAGVLSPSGH120 HSSQHQGPVG LGQGSEKGWQ EVPRSSQPGR GTNALNTSKL RDPKVSTPGS GLPPHRH 177

(2)	) INFORMATION	ON	SEQ	ID	NO.	275:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

QFPGPSVPEQ STSVSVTTSC LFPSLHLLQF IYMLLLLVHF CLPYQAVNEG RNLVCFIHHH60 VPSAWHIVGL H

- (2) INFORMATION ON SEQ ID NO. 276:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

FFFFFFFFF FFFCLINMSI YLAPDGNTKS WQWEWKGSLS QILPYYVDPK AGLGSKAHKP 60 PKQIFIEHLD YYRPSILLGT MGDVKEVISH MICLQGAKNA SG 102

- (2) INFORMATION ON SEQ ID NO. 277:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 65 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GVIESRRVLS RGVIRFIFKQ PNPGRCGPIL SALKKIPFPY LPASIMSVEE SNCGSFEGDG60 PFFPV 65

- (2) INFORMATION ON SEQ ID NO. 278:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 65 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FFFFFFFF FFLFNKYEHL FGTRWQYKIL AVGVERFSLS NTSILCRPKG RTWQQGSQTT60 QTNIY

- (2) INFORMATION ON SEQ ID NO. 279:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 489 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LADSFPGSSP YEGYNYGSFE NVSGSTDGLV DSAGTGDLSD GYQGRSFEPV GTRPRVDSMS 60
SVEEDDYDTL TDIDSDKNVI RTKQYLYVAD LARKDKRVLR KKYQIYFWNI ATIAVFYALP120
VVQLVITYQT VVNVTGNQDI CYYNFLCAHP LGNLSAFNNI LSNLGYILLG LLFLLIILQR180
EINHNRALLR NDLCALECGI PKHFGLFYAM GTALMMEGLL SACDHVCPNY TNFQFDTSFM240
YMIAGLCMLK LYQKRHPDIN ASAYSAYACL AIVIFFSVLG VVFGKGNTAF WIVFSIIHII300
ATLLLSTQLY YMGRWKLDSG IFRRILHVLY TDCIRQCSGP LYVDRMVLLV MGNVINWSLA360
AYGLIMRPND FASYLLAIGI CNLLLYFAFY IIMKLRSGER IKLIPLLCIV CTSVVWGFAL420
FFFFQGLSTW QKTPAESREH NRDCILLDFF DDHDIWHFLS SIAMFGSFLV LLTLDDDLDT480
VQRDKIYVF

- (2) INFORMATION ON SEQ ID NO. 280:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

APLCHRPVTL SCCGDESQHR CPALDGSRTA RSSLGLAWDS HGVAWNLAAA LCRGAGLLPW 60 DPQMLAKLLL SSQCWGLPWA PVLWLSICPF ARGRMEGTPS PFHALHFARP PPHNAPAWDL120 RPLFPPILPL QGLVWGLNLC PVSGPQFSLG CPWLPSLPIP VSQDGWGYEI LGVGQLVPDF180 WC

- (2) INFORMATION ON SEQ ID NO. 281:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 536 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ARPGCPAAIQ CWAAVLGLIP TARQSDRSMT QRSSGPLEVK RRAQLLLEDI DLVPLHSIQV 60 VIQCQQHQEG PEHGDGGEV PDVVVVKEVE EDAVPVVLPR LCRGFLPGAE SLEEEEEREA120 PDHGGANDAE QGDELDPLPT PELHDDVEGE VKEQVADANG QQVGSEIIGA HDKPIGSQRP180 VDDVAHDQQH HAVHVERPAA LPDAVCVEHV EDAAEDPRVQ FPPAHVIELR AEEQGGDDVN240 DGEDDPERRV PFAKDHAQHR EEDDNGQAGV GTVGAGVDVR VPLLVELQHA ESGDHVHERC300 VKLEIGIVGA HMIASTEQPL HHQGCAHGVE KPKVFGDPTF QGTEVIAQQG PVVVDLPLQD360 DEQEKQPQQD VPQVAEDVVE GAEIAQWVGA EEVVVADVLI PCDIHHRLVG DHQLHHRKGI420 EDSNGGNVPE VDLVLFPQNT LVLPCQVSHI EVLLGANDIL VGIDVGQCVV VILLHRAHGV480 HSGPSTYRFK GAALVTVREV PSASAVNQTI GRSRNILKGA IVVTLIRGTA RKRISQ 536

- (2) INFORMATION ON SEQ ID NO. 282:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 551 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

PLSSPSCCRY RRCCRRLRPP LRSVVQPGPR TMSLSRSEEM HRLTENVYKT IMEQFNPSLR 60
NFIAMGKNYE KALAGVTYAA KGYFDALVKM GELASESQGS KELGDVLFQM AEVHRQIQNQ120
LEEMLKSFHN ELLTQLEQKV ELDSRYLSAA LKKYQTEQRS KGDALDKCQA ELKKLRKKSQ180
GSKNPQKYSD KELQYIDAIS NKQGELENYV SDGYKTALTE ERRRFCFLVE KQCAVAKNSA240
AYHSKGKELL AQKLPLWQQA CADPSKIPER AVQLMQQVAS NGATLPSALS ASKSNLVISD300
PIPGAKPLPV PPELAPFVGR MSAQESTPIM NGVTGPDGED YSPWADRKAA QPKSLSPPQS360
QSKLSDSYSN TLPVRKSVTP KNSYATTENK TLPRSSSMAA GLERNGRMRV KAIFSHAAGD420
NSTLLSFKEG DLITLLVPEA RDGWHYGESE KTKMRGWFPF SYTRVLDSDG SDRLHMSLQQ480
GKSSSTGNLL DKDDLAIPPP DYGAASRAFP AQTASGFKQR PYSVAVPAFS QGLDDYGARS540
MSSADVEVAR F

- (2) INFORMATION ON SEQ ID NO. 283:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 185 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGEAAGQPGS PPSHQLAKCP PLTQGYPRLH GHVTRGVYPQ EAAPQPWAAQ PLGLALQGPA 60 PHSARPCLEQ LGSSPGQTQV GQDQAAGAWM FSTQERTDDD RTGYMGRAGE ATRWAALQMW120 PSAEEGGRPV VGHCRLQLDV GKGILTLVRR LRIWPLPHRR CSWTALHSHP GPGRRARPH180 CRASA

- (2) INFORMATION ON SEQ ID NO. 284:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 518 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

SGGSESGHFH IGAAHGPRSI VIQALGEGGH GHTVGPLLEA AGRLGGEGPG GGAVIGGWDG 60
QVVLVQEVAR AAALPLQAH VQPVTAIAVQ DPGVGEGKPA PHLGLLTLSV VPAIAGLRHQ120
QGNEVTLLEA QEGAVVPSSV GEDGLHPHTA IALQAGCHGA RARQSLVLGG GIAVFWGHAL180
AHGECVGVGV AELALRLRRR QGFGLGSLAV SPRAVVLAIR ACDAVHDGCA LLGRHPPHER240
CQLGGHRQGL GPRNGVGNDQ VGLGGRQGAG EGGAVAGHLL HELHRALRDL AGVGTGLLPQ300
RQLLRQQLLA LGVVGRGVLG HGALLLHQEA EAPALLCQCG LVAVGHVILQ LALLVADGVD360
VLQLLVRVLL RILAALALLP KLLQLSLTLV QGVAFAPLLS LVFLQRSTQI PGVQLHLLQ420
LRKQLVVKRL QHFFQLILDL PVDFSHLEEN VSEFFGALAL AGQLPHLHQG VKVAFGCIRH480
TCQCLLVILP HGDEVPEARV ELLHDGLIDI FREPVHLL

- (2) INFORMATION ON SEQ ID NO. 285:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 217 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

VREAARREQR YQEQGGEASP QRTWEQQQEV VSRNRNEQES AVHPREIFKQ KERAMSTTSI 60 SSPQPGKLRS PFLQKQLTQP ETHFGREPAA AISRPRADLP AEEPAPSTPP CLVQAEEEAV120 YEEPPEQETF YEQPPLVQQQ GAGSEHIDHH IQGQGLSGQG LCARALYDYQ AADDTEISFD180 PENLITGIEV IDEGWWRGYG PDGHFGMFPA NYVELIE

- (2) INFORMATION ON SEQ ID NO. 286:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 162 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

AGASGRLWLP SAFICLFSFS LASKGWWPPL FRMTLGNSER RELFLAEFVT KVRVDHGGLA 60 AGNLSCWSLL CAPHSISLSL CLGYGKWGCR WPSSHPGYSK TADTTCSSTR LTRCLQAPVC120 ASTDSDFRKS NTEWPWPVVF PYFLSQLIRV SEEQICFWTK KK 162

- (2) INFORMATION ON SEQ ID NO. 287:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 173 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LLACRGWPGR RWWEELNSGK VMYAFCRVKD PNSGLPKFVL INWTGEGVND VRKGACASHV 60 STMASFLKGA HVTINARAEE DVEPECIMEK VAKASGANYS FHKESGRFQD VGPQAPVGSV120 YQKTNAVSEI KRVGKDSFWA KAEKEEENRR LEEKRRAEEA QRQWSRSAGS VSA 173

- (2) INFORMATION ON SEQ ID NO. 288:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 597 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

EKCGQYIQKG YSKLKIYNCE LENVAEFEGL TDFSDTFKLY RGKSDENEDP SVVGEFKGSF 60 RIYPLPDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQPQDNNGLC DPYIKITLGK120 KVIEDRDHYI PNTLNPVFGR MYELSCYLPQ EKDLKISVYD YDTFTRDEKV GETIIDLENR180 FLSRFGSHCG IPEEYCVSGV NTWRDQLRPT QLLQNVARFK GFPQPILSED GSRIRYGGRD240 YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGKLQMWV300 DVFPKSLGPP GPPFNITPRK AKKYYLRVII WNTKDVILDE KSITGEEMSD IYVKGWIPGN360 EENKQKTDVH YRSLDGEGNF NWRFVFPFDY LPAEQLCIVA KKEHFWSIDQ TEFRIPPRLI420 IQIWDNDKFS LDDYLGFLEL DLRHTIIPAK SPEKCRLDMI PDLKAMNPLK AKTASLFEQK480 SMKGWWPCYA EKDGARVMAG KVEMTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540 SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLLFVAVL LYSLPNYLSM KIVKPNV 597

- (2) INFORMATION ON SEQ ID NO. 289:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

DQHSCFKMSP DSKASHNPSF PKMGVESDME DETTAWMNLK PTKSCTSTSG PLKSGLLFTS 60 SGLRGWSLST WKQGLCTAPS SPTFPRENFR CGWMFSPRVW GHQALLSTSH PGKPRNTTCV120

- (2) INFORMATION ON SEQ ID NO. 290:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 289 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60 FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120 CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180 PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240 NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNFQVFFLR 289

- (2) INFORMATION ON SEQ ID NO. 291:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 201 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GTGDGSKEIN IVWGIQVPIF HNGPWVSTNH PVARFPRITS LASEGIIVPS TSTIRGMGVW 60 RASCGDCRAD STSSIAQDRG PGLTIGHQAL GSLVWVGESW GQTWGEYLGG PRWLGWLDLR120 QSWALSISEE VVKKRDFLFH FLNFLCMLVE DMFAHKLRTL EFLATERTQP LILAQFLRVG180 GDELLHFLLW VFAPHLLGLF L

- (2) INFORMATION ON SEQ ID NO. 292:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 171 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SVIFFKIGFC EGRLVGRGGV PGSEAQSCVL SSSVWISLAA SLMSLRTICL CWVMPLMLRT 60 RRVRSLFTPG LSSHSRRRMF CRFQQISLML TLRSKVTQPR RKNLLSGWGS ESATRIKPGY120 LLQREMISAR EMLGAMLRMK REQVLCSGRG LHSSPAASLG FSHSSSLGFS F 171

- (2) INFORMATION ON SEQ ID NO. 293:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 485 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

EKEKPKEEEW EKPKDAAGLE CKPRPLHKTC SLFMRNIAPN ISRAEIISLC KRYPGFMRVA 60
LSEPQPERRF FRRGWVTFDR SVNIKEICWN LQNIRLRECE LSPGVNRDLT RRVRNINGIT120
QHKQIVRNDI KLAAKLIHTL DDRTQLWASE PGTPPLPTSL PSQNPILKNI TDYLIEEVSA180
EEEELLGSSG GAPPEEPPKE GNPAEINVER DEKLIKVLDK LLLYLRIVHS LDYYNTCEYP240
NEDEMPNRCG IIHVRGPMPP NRISHGEVLE WQKTFEEKLT PLLSVRESLS EEEAQKMGRK300
DPEQEVEKFV TSNTQELGKD KWLCPLSGKK FKGPEFVRKH IFNKHAEKIE EVKKEVAFFN360
NFLTDAKRPA LPEIKPAQPP GPAQILPPGL TPGLPYPHQT PQGLMPYGQP RPPILGYGAG420
AVRPAVPTGG PPYPHAPYGA GRGNYDAFRG QGGYPGKPRN RMVRGDPRAI VEYRDLDAPD480
DVDFF

- (2) INFORMATION ON SEQ ID NO. 294:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 368 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ESSGFQAIGR AEDDARSCWV KTSESTRPYQ LLRRRRPTLI TYRIFRHRRH KDTSSGDHLT 60 CRLDPQAKDL KDGTQEEATK RQEAPVDPRP EGDPQRTVIS WRGAVIEPEQ GTELPSRRAE120 VPTKPPLPPA RTQGTPVHLN YRQKGVIDVF LHAWKGYRKF AWGHDELKPV SRSFSEWFGL180 GLTLIDALDT MWILGLRKEF EEARKWVSKK LHFEKDVDVN LFESTIRILG GLLSAYHLSG240 DSLFLRKAED FGNRLMPAFR TPSKIPYSDV NIGTGVAHPP RWTSDSTVAE VTSIQLEFRE300 LSRLTGDKKF QEAVEKVTQH IHGLSGKKDG LVPMFINTHS GPVSPTWGVF HGGAPGADSL360 LLSYLFER

- (2) INFORMATION ON SEQ ID NO. 295:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

ALRSPPRMRI VLSNRLTSTS FSKCNFFDTH FLASSNSFLR PKIHMVSSAS ISVRPRPNHS60 LKDLDTGFSS SWPHANLRYP FHACRKTSIT PFWR 94

- (2) INFORMATION ON SEQ ID NO. 296:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

LLRHPLPGFL KFFPQTQDPH GVQRVDQCET EAKPLTEGPG HRLQLVMAPC KLAVSFPCMQ60 EDVNHALLAI VQMHWCALCP GRWQGRLGGH FCSS 94

- (2) INFORMATION ON SEQ ID NO. 297:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

SGPLLAGPAT LTGRMSEVRL PPLRALDDFV LGSARLAAPD PCDPQRWCHR VINNLLYYQT 60

NYLLCFGIGL ALAGYVRPLH TLLSALVVAV ALGVLVWAAE TRALCAAAAA ATLQPAWPQC120 LPSASWCSGS RAALAPSCSA SPGRCF 146

- (2) INFORMATION ON SEQ ID NO. 298:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 152 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TQRHSHPPFS MLIPKLGPGA RHSQILNPGP KLFQTPPYLP TQVKTLPNLE LRTQVFHAPV 60 WMESGILTVG PLVQVIPTLT SPICLPPALL RHFAPHPNVP HHRQPRGEVG TGLSREWGVY120 VSVAATIKPV ASLMPKKKKK STGRKYSSSS RP 152

- (2) INFORMATION ON SEQ ID NO. 299:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 172 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RTTTTTIFAA GRLFFFFWHE RCNRLYCCSN TNIYAPFPAE ACPHLTPWLS MVWNIGVRGK 60 MPKQSWREAN GTGEGRDHLD QGSNSQDTRL HPHRGMEHLG SEFKIWQCLD LGWKVGWGLE120 KLWSRVQDLR VPCSRPQFGD EHGEGWMGVS LGSQFEIGHG CSGLKPOFWG WM 172

- (2) INFORMATION ON SEQ ID NO. 300:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 178 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

WFWRESYWQT IKVDLQVEHP YQFLLKYAKQ LKGDKNKIQK LVQMAWTFVN DSLCTTLSLQ 60 WEPEIIAVAV MYLAGRLCKF EIQEWTSKPM YRRWWEQFVQ DVPVDVLEDI CHQILDLYSQ120 GKQQMPHTP HQLQQPPSPE PPTPLPGPCG CWASHLKEGK VVQPEPVEQC PVWPPKPK 178

- (2) INFORMATION ON SEQ ID NO. 301:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CISQDVCANL KYKNGPPNPC IGDGGSSLFK MSRSTFWKTS ATKSWIFTHK ENNRCLITPP 60 ISCNSPHLLS LPPRCLGPVV AGPPTSRRGR LYSPNPWSNA LSGLQNQNKT GSL 113

- (2) INFORMATION ON SEQ ID NO. 302:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 90 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

GGRPSNHRAQ AAGWEAQEMG AVAADGGCDE ASVVFLVSKD PGFGGRCLPK RRPGHLEQTA60 PTISYTWVWR SILVFQICTN VLRDTSLLLL 90

# (2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 158 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

TQVMVQSMFA PTDTSDMEAV WKEAKPEDLM DSKLRCVFEL PAENDKPHDV EINKIISTTA 60 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRLRE ENKQFKEEDG LRMRKTVQSN120 SPISALAPTG KEEGLSTRLL ALVVLFFIVG VIIGKIAL

## (2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

VNKALPFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSQGADGL DRTEDTESSL 60 GREWATWGLL CGADRTPQHA GLQLPKGQHQ QARKGVILRE VIQHHVPRPT NV 112

## (2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

FKGKTCEMSS YINFFLHMVM INLNPMIWWI HQSNLPSCAC YLYKAIFPII TPTIKNKTTR 60 AKSRVLRPSS FPVGANAEMG LLLCTVFLIR SPSSSLNCLF SSRSL

- (2) INFORMATION ON SEQ ID NO. 306:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

RPPQRTLRHS AQLGAAPAAL PQPLWELPRA HGSQRQPGPG EAADHAEQER EEAAERPGSS 60 PEEGQEGSGA FGGHTGHRAC ARCLGRGALG GRIPCGLLCQ LFRRDGCPAD SEVQHHIHQH120 WQQLLP 126

- (2) INFORMATION ON SEQ ID NO. 307:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 240 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
      - (D) TOPOLOGY: linear
  - MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

NVGRCCEAQA RAGAASLNAS LDGLHNALFA TQRSLEQHQR LFHSLFGNFQ GLMEANVSLD 60 LGKLQTMLSR KGKKQQKDLE APRKRDKKEA EPLVDIRVTG PVPGALGAAL WEAGSPVAFY120 ASFSEGTAAL QTVKFNTTYI NIGSSYFPEH GYFRAPERGV YLFAVSVEFG PGPGTGQLVF180 GGHHRTPVCT TGQGSGSTAT VFAMAELQKG ERVWFELTQG SITKRSLSGT AFGGFLMFKT240

- (2) INFORMATION ON SEQ ID NO. 308:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

KAGIEGHRGS CLPERRAQGT WHRPCDPYVH QRLRFLLVPL PGSFQVFLLL LPFPAQHGLQ 60 LPQVQADVGF HEPLEVPKEA VEEPLVLLQA ALSGEECVVE AVKGGVEGGG PGPGLGLAAP120 PDI

- (2) INFORMATION ON SEQ ID NO. 309:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 84 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

PTTTLVIPLF FLSSRKRKQK DSFQTALCSL HCSFPKQAAS TGKAHVVTPY FSEVLLFHGV60 TLLSESKFRK QVLPLADKNH TSFL 84

- (2) INFORMATION ON SEQ ID NO. 310:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CDRVPLFLSY WCAVADSWLT ASSVSHVKGI LSPQPTECAP PGPANCFFNF FFFFFLVET 60 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQPEQD DLNLINSTPK QQLSLSQGCQ120 GGLCEGKD

- (2) INFORMATION ON SEQ ID NO. 311:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRYLYKKLV WFLSAKGKTC FLNLLSDNKV60 TPWKRRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

- (2) INFORMATION ON SEQ ID NO. 312:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:	
ISTSIAALWL PGGQDAGGGA LWPLCGSRGL CVSDRFPGNF RARLTSWKFK YSIALEF 57	٠
(2) INFORMATION ON SEQ ID NO. 313:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 52 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:	
SAHQLQHCGY QGVRMRAVEP SGLCVVAEDS VSATVFRETS GRDSHLGNSN TQ	5.2
(2) INFORMATION ON SEQ ID NO. 314:	`
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 43 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:	

NSRAIEYLNF QDVSLARKFP GKRSLTQSPR LPHKGQRAPP PAS

- (2) INFORMATION ON SEQ ID NO. 315:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 247 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60 HNWGTVKDEL TESPKYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKSE EAHAEDSVMD180 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGGRG PNRGSRTDKS SASAPDVDDP240 EAFPALA

- (2) INFORMATION ON SEQ ID NO. 316:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

FMKNKSLLPL PISTFIWFSD IKFYFCPVLI LNSLPLIQSH LFWTLLFYLF NFILLIFSVC60 HWMMFFTFRC FLSHI 75

- (2) INFORMATION ON SEQ ID NO. 317:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

SFGILKHAKA LNRRVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60 VHLVLPCRHV LGGQGLQN 78

- (2) INFORMATION ON SEQ ID NO. 318:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 235 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

LHLGAQRALA PGLFRLQGML RALLGRQLFR ARGPPVVREP LPRTTRLAVR HVWPPCDRPL 60 RVGPGSPLPP GPLHMHLLPA PAHQGVLPGA RRQALLPALL PEALRLTARS ARPLPRRPRP120 PGKAGSSRPR GLALRAGGPT HWRAPPLRYY ESSGVKFRNG PARPKPTRPQ SGLHTDKNSR180 AGLHSIPTLE GAPLLGEGPC NSSESEARPG RPCSLHPHCS VHFFYLHKHT HSTSK 235

- (2) INFORMATION ON SEQ ID NO. 319:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 478 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

GSRPPPCSPR ATGPRPAMED LDALLSDLET TTSHMPRSGA PKERPAEPLT PPPSYGHQPQ 60
TGSGESSGAS GDKDHLYSTV CKPRSPKPAA PAAPPFSSSS GVLGTGLCEL DRLLQELNAT120
QFNITDEIMS QFPSSKVASG EQKEDQSEDK KRPSLPSSPS PGLPKASATS ATLELDRLMA180
SLSDFRVQNH LPASGPTQPP VVSSTNEGSP SPPEPTGKGS LDTMLGLLQS DLSRRGVPTQ240
AKGLCGSCNK PIAGQVVTAL GRAWHPEHFV CGGCSTALGG SSFFEKDGAP FCPECYFERF300
SPRCGFCNQP IRHKMVTALG THWHPEHFCC VSCGEPFGDE GFHERGRPY CRRDFLQLFA360
PRCQGCQGPI LDNYISALSA LWHPDCFVCR ECFAPFSGGS FFEHEGRPLC ENHFHARRGS420
LCATCGLPVT GRCVSALGRR FHPDHFTCTF CLRPLTKGSF QERAGKPYCQ PCFLKLFG 478

- (2) INFORMATION ON SEQ ID NO. 320:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 285 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

EQGLGVWRTR LFREGAASGG EGEPSGLSAE ELQEAGLAVG LAGALLEGPL GERAQAEGAC 60
EVVRVEAATQ GRHAAAGHRE ATRGAQRAAS CVEVVLAQRA ALVLEKAASR EGREAFPADE120
TVRVPERAER RDVVIQDGAL AALAARGEQL QEVPAAVGAA LALVETLISE GLPATDAAEM180
LWVPVSAQGG HHLVSDGLVA EATSWREALK VALGAEGGSI LLEEAAASQG GGTASANEVL240
GVPGAAQSRH HLPSNRFIAG ATEAFGLGGN TPAAEVGLQQ PQHGV 285

- (2) INFORMATION ON SEQ ID NO. 321:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GLHLQPLLWR QSTEEEVREE GQALTEPKSC GAQGGAQHRG LTPCPTGNGL GLAQPKIPAL60 SNSWRVDSVL ACLVSSDIFH TVEQNHQPCT DVTLCRKRP

- (2) INFORMATION ON SEQ ID NO. 322:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

ETQSSQRLTC PRSLGLDLSL RLRLQNPHSI CYISQGWGQG SCEQKEKYQL LKGLGFVGRA60 RQGQRGIQNK GASTSAWDGP IHSGRGCGVS PVLRNHLAS 99

- (2) INFORMATION ON SEQ ID NO. 323:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 83 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

SNPKAPVSMW VKGPTMGTYT QEDESSLASE SDCLPQTPPQ NRLLSHLPLH SDKTQAHIPG60 PGVFACICID GNAGPAKAFF YIK 83

- (2) INFORMATION ON SEQ ID NO. 324:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 111 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

VFPTVLRGVL VPSSVTSKPG LIVPIGDEGG MRRSHLQLLS VERTSGTEKN RGPHGSLEGR 60 GTRVGELIAE RRDVQRPSAP LSWDVNRIFP STPSLPPVLP LFFFPSIKRC I 111

- (2) INFORMATION ON SEQ ID NO. 325:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 272 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

SSRASGITRA ARPCPAKNEG PSKAFVNCDE NSRLVSLTLN LVTRADEGWY WCGVKQGHFY 60 GETAAVYVAV EERKAAGSRD VSLAKADAAP DEKVLDSGFR EIENKAIQDP RLFAEEKAVA120 DTRDQADGSR ASVDSGSSEE QGGSSRALVS TLVPLGLVLA VGAVAVGVAR ARHRKNVDRV180 SIRSYRTDIS MSDFENSREF GANDNMGASS ITQETSLGGK EEFVATTEST TETKEPKKAK240 RSSKEEAEMA YKDFLLQSST VAAEAQDGPQ EA 272

- (2) INFORMATION ON SEQ ID NO. 326:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 241 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TLVFGRLRTK PFRIPGFLQR KRRWQIQEIK PMGAEHLWIP AALRNKVEAP ERWSPPWCPW 60
AWCWQWEPWL WGWPEPGTGR TSTEFQSEAT GQTLACQTSR TPGNLEPMTT WEPLRSLRRH120
PSEEKKSLLP PLRAPQRPKN PRRQKGHPRR KPRWPTKTSC SSPAPWPPRP RTAPRKPRRC180
RRLLPAPMTI TFRIMSILGP SAPGDPTPCS NTCLGFSYCP QRRAGPLLSD IKAWPNCSYW240
G

- (2) INFORMATION ON SEQ ID NO. 327:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 121 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

AVVRVTWYKG EGITLPPVLT PALVRGESIP IRLFLAGYEL TPTMRDINKK FSVRYYLNLV 60 LIDEEERRYF KQQEVVLWRK GDIVRKSMSH QAAIASQRFE GTTSLGEVRT PSQLSDNNCR120

- (2) INFORMATION ON SEQ ID NO. 328:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRLPC 60 THLPWWAGFS LLGSTLPPSV HDTDPRASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120 GQKEVACGNL RSPHPRFPKR 140

# (2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSGSSE SQEPRMRALC 60 SPSSKTQGSP PRKGAHVPQR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120 DLFSGCK

- (2) INFORMATION ON SEQ ID NO. 330:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 418 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GSTSTKNTKI SQACGVIVEL IKSKKMAGGA VLLAGPPGTG KTALALAIAQ ELGSKVPFCP 60 MVGSEVYSTE IKKTEVLMEN FRRAIGLRIK ETKEVYEGEV TELTPCETEN PMGGYGKTIS120 HVIIGLKTAK GTKQLKLDPS IFESLQKERV EAGDVIYIEA NSGAVKRQGR CDTYATEFDL180 EAEEYVPLPK GDVHKKKEII QDVTLHDLDV ANARPQGGQD ILSMMGQLMK PKKTEITDKL240 RGEINKVVNK YIDQGIAELV PGVLFVDEVH MLDIECFTYL HRALESSIAP IVIFASNRGN300 CVIRGTEDIT SPHGIPLDLL DRVMIIRTML YTPQEMKQII KIRAQTEGIN ISEEALNHLG360 EIGTKTTLRY SVQLLTPANL LAKINGKDSI EKEHVEEISE LFYDAKSSAK ILGLTRQG 418

- (2) INFORMATION ON SEQ ID NO. 331:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VPQCGLGANL PQVVQCLLTD VDSFRLGTDF NDLFHFLWSI QHGPDYHHSV QKVKRDAVRG 60 CDVLSASDDT VASVGCKDDD GSDRRLQGAV QVGEALNVQH VDLINKQHTR DQLSNALVDV120 LVHHLINLPS KFVCDFCLLW LH

- (2) INFORMATION ON SEQ ID NO. 332:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LAHHGQDILS PLGPRISHIQ VMQGHILDDF FLFVHIPFWQ GDILFSFKVE FCGIGITPAL 60 PLHGPTVGFN VNHISSFYSL FLQTFKNAGV QFQLFGSFGC FESYDHMANG FAISSHGILC120 LTRS

- (2) INFORMATION ON SEQ ID NO. 333:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 176 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

QAMGKKQKNK SEDSTKDDID LDALAAEIEG AGAAKEQEPQ KSKGKKKKEK KKQDFDEDDI 60 LKELEELSLE AQGIKADRET VAVKPTENNE EEFTSKDKKK KGQKGKKQSF DDNDSEELED120 KDSKSKKTAK PKVEMYSGSL TNFLKKLKGK LKNQIRSGMG QRRMRITVKK LKSVQE 176

- (2) INFORMATION ON SEQ ID NO. 334:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

RFKIKKDCKT ESGNVLWEFN KLPKKAKGKA QKSNKKWDGS EEDEDNSKKI KERSRINSSG 60 ESGDESDEFL QSRKGQKKNQ KNKPGPNIES GNEDDDASFK IKTVAQKKAE KKERERKKRD120 EEKAKLRKLK EKEELETGKK DQSKQKESQR KFEEETVKSK VTVDTGVIPA SEEKAETPTA180 AEDDNEGDKK NER

- (2) INFORMATION ON SEQ ID NO. 335:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

ETVAFARPFF PSLFSFPPLS SFLFLLIFRS FCLLHCHLLQ LWESLLSLQR QELLQYQQSL 60 WILOFLLQIS FEIPFVYSDP FYLFLTLLFL SASAVSLFLH LAFFSRAPSF LPSFGPLS 118

- (2) INFORMATION ON SEQ ID NO. 336:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 230 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

LQRLLPPGAE RPAHLCTGPG GEDGAGGRVP GTRPQRPPAL QRAEDGRQGG LRVAGTAGPP 60
PGVPLRPGQG GSGHQEQGAS HPGSLDQGLT GAKRPQGCPA CGRRPPCVGG VPGSAHRPQP120
EGAALRGRS RLQQAGPCCC RVLWLRRCHP AGLPRRPPAA DPGARAAAGG RHVLCRSPLH180
PGLRPPLPQW GLLRPEGGCL CVPVSRGILR TALREGAGGE VSGGRGYLGL 230

- (2) INFORMATION ON SEQ ID NO. 337:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 416 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

QDGSGPFLAD FNGFSHLELR GLHTFARDLG EKMALEVVFL ARGPSGLLLY NGQKTDGKGD 60
FVSLALRDRR LEFRYDLGKG AAVIRSREPV TLGAWTRVSL ERNGRKGALR VGDGPRVLGE120
SPVPHTVLNL KEPLYVGGAP DFSKLARAAA VSSGFDGAIQ LVSLGGRQLL TPEHVLRQVD180
VTSFAGHPCT RASGHPCLNG ASCVPREAAY VCLCPGGFSG PHCEKGLVEK SAGDVDTLAF240
DGRTFVEYLN AVTESEKALQ SNHFELSLRT EATQGLVLWS GKATERADYV ALAIVDGHLQ300
LSYNLGSQPV VLRSTVPVNT NRWLRVVAHR EQREGSLQVG NEAPVTGSSP LGATQLDTDG360
ALWLGGLPEL PVGPALPKAY GTGFVGCLRD VVVGRHPLHL LEDAVTKPEL RPCPTP 416

- (2) INFORMATION ON SEQ ID NO. 338:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 241 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

NQHMKNTAMA RPRYPGRRQR STPSHSELLS IAPRRAWGVA EGYGHVQGGW AGPAEGQDTQ 60
IGPGLASAPQ QPGLAQAARE QRRAVPSSNI VWKSQYWRRR PRQGPEHTQE GAAQIGAWKG120
PVGSPGGRAP SDLSSPFLSG TRVPPDGARV IQEPGLLPGG DTVGQAQCKA GAQHLEAGVC180
VLRLPSTPSP PRCHLACPSL STRSVCSTAA WTEGRPGQQS LRPTLRQENH IKKRQVYKNR240
K

- (2) INFORMATION ON SEQ ID NO. 339:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

LLQPQGEMPP GNPPMSTRGQ EATVLRTPEN LAGELFLVHP SLQLYLCPAD NVKDWSKVVL60 AYEPVWAIGT GKTATPQQG 79

- (2) INFORMATION ON SEQ ID NO. 340:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 62 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

FPVGVLQSCQ YQWPTQAHRP GRPCSSPSRY LQGRDTAGGK GEQERALQPG SPEYEERWPP60 AP

- (2) INFORMATION ON SEQ ID NO. 341:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

SLLGCCSLAS TNGPHRLIGQ DDLAPVLHVI CRAEIQLEGR VNKKELSSQV LRSTKNGGLL60 PPSGHWGISR WHLPLGLEKS 80

- (2) INFORMATION ON SEQ ID NO. 345:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 257 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

KNLSQLEPRE NAKEEVRKER GMGWVAAGAA QLLSLLSTST ASDSSVISSS ACTSGLLPRR 60 RSPASPRSAH LHHLGGLEHF HLALADLLDV EGEGWHLVDR GLGARVHHVV GREGFAQLVP120 RRLQFLAPLG GHQARAQLVH ALLQGVPRLL QVFLGLEARL LQVLAGTHLG LLHLLLGEGL180 LEVVHAPQAL RLIRSARDSS ITSSTSTASS DESSSAAASS SGRSPSPSSS PSFSGSASDS240 FSDLLMLSLA GSFTSSW 257

- (2) INFORMATION ON SEQ ID NO. 346:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 237 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN ·
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

KSRRRCQRRR ARSWARASGP RRTQRRWSFR RTRRWRLRRL LRSPAQSVSS AGPAARGRLQ 60 EGLLQGEDGE DQGAYPREPG EDAPQDQGKP GEDAAHPGEA HEQAGHAPGA RRAARETEDV120 AGQVAQILHA RPRGVRALQD RGLQGATLHL PRQEDPRGPG GSAQGHRDGG GGRSGGRPAT180 CGAGAAPTCT RCWRSPRSRT PCWWTRATAT ERPPLPPTPF LAPSELPLSH SLSARAG 237

- (2) INFORMATION ON SEQ ID NO. 347:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 263 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60 TQAQLEERQA EMEGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSLER120 QAGQIKKLEV NEAELLRRRN FKVMIYQDEV KLPAKLSISK SLKESEALPE KEGEELGEGE180 RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSRRPSPRRR WRRPRCVPAR240 TWRRRASRPR KTWRRRGTPW RSA

- (2) INFORMATION ON SEQ ID NO. 348:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

SSGSSRFGSS GSRRRYASLY FCCAIEDQDN ELITLEIIHR YVELLDKYFG SVCELDIIFN 60 FEKAYFILDE FLLGGEVQET SKKNVLKAIE QADLLQEEAE TPRSGS 106

- (2) INFORMATION ON SEQ ID NO. 349:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

LFLMPQNKVR MVICQEFFIT VSYKKRVALF TVLCVKSLFK ARMFPLGYLL KLNLFCFPPL60 RSAAHFTAAS FLSMALPS 78

- (2) INFORMATION ON SEQ ID NO. 350:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 65 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TCLHGLYFHL YMLGWIKLCC DCDQHSGHVS TVLSHRQLVV INVQRTKKKK GAASLGGITG60 SGVKR

- (2) INFORMATION ON SEQ ID NO. 351:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 196 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

LPGLPLRQLG GVCHGHRPGL LLHQQHGGGA GAVQQPQREE EALHDPGQGS APAELCQFQQ 60 HVPRFPLQQP QAVQEGGAG AGQGLVLWQP GAGLQGVQPG DDGAPDLQHG DAAGDSHHDD120 PAQELPAAEH RAQGPGGPRP ALRGGARSNC RVCLVQMCPE APEGSHQLMP ASDPQQGWFA180 AAAQGEPVSD PGHHHH

## (2) INFORMATION ON SEQ ID NO. 352:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 361 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

SLASLSDSLG VSVMATDQDS YSTSSTEEL EQFSSPSVKK KPSMILGKAR HRLSFASFSS 60
MFHAFLSNNR KLYKKVVELA QDKGSYFGSL VQDYKVYSLE MMARQTSSTE MLQEIRTMMT120
QLKSYLLQST ELKALVDPAL HSEEELEAIV ESALYKCVLK PLKEAINSCL HQIHSKDGSL180
QQLKENQLVI LATTTDLGV TTSVPEVPMM EKILQKFTSM HKAYSPEKKI SILLKTCKL1240
YDSMALGNPG KPYGADDFLP VLMYVLARSN LTEMLLNVEY MMELMDPALQ LGEGSYYLTT300
TYGALEHIKS YDKITVTRQL SVEVQDSIHR WERRRTLNKA RASRSSVQPL HLRVVPGARA360
A

# (2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 161 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

VDGFLQGLQD TFVQGRLYNC FELLLGVQGG VHQGLELGAL QQVALELGHH GANLLQHLRA 60 GGLARHHLQA VHLVVLHQAA KVRALVLRQL HHLLVQLAVV GEESVEHAAE TGKAQPVPSL120 AQDHGGLLLH AGAAELLQLL LRAAGGVGVL VGGHDRHPQA V

- (2) INFORMATION ON SEQ ID NO. 354:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 218 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

SGRGPKYVID VEQPFSCTSL DAVVNYFVSH TKKALVPFLL DEDYEKVLGY VEADKENGEN 60 VWVAPSAPGP GPAPCTGGPK PLSPASSQDK LPPLPPLPNQ EENYVTPIGD GPAVDYENQD120 VASSSWPVIL KPKKLPKPPA KLPKPPVGPK PEPKVFNGGL GREAASSVSA QPLLSPQAGL180 GRHGRQSYRR SWEKRRGTGS MVSDTPGTSG LVPGRARW 218

- (2) INFORMATION ON SEQ ID NO. 355:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 253 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

AGEGVDGLTQ ETPLKPVSQL PGPAGAPTGR RGQAEDPGSV MASALRPPRV PKPKGVLPSH 60 YYESFLEKKG PCDRDYKKFW AGLQGLTIYF YNSNRDFQHV EKLNLGAFEK LTDEIPWGSS120 RDPGTHFSLI LRNQEIKFKV ETLECREMWK GFILTVVELR VPTDLTLLPG HLYMMSEVLA180 KEEARRALET PSCFLKVSRL EAQLLLERYP ECGNLLLRPS GDGADGVGHH AADAQRDARG240 PALQGEAGGA PST

(2) INFORMATION ON SEQ ID NO. 356:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

LTTASREVQE NGCSTSITYL GPLPLHLVMP DHVRPVVHLP RGDRHRRRRP RWAAAAGSRT 60 RGSAPGAVVP PAGSPSGSTR VSPVHGAPPL WPRLQTSCIG AQEAGSSRSG HGAPPPLR 118

- (2) INFORMATION ON SEQ ID NO. 357:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 223 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

DHTCGCAGNL QEAIMLRSGV TSQGIHPGSP WCCTPTQAEL IVGDQSGAIH IWDLKTDHNE 60 QLIPEPEVSI TSAHIDPDAS YMAAVNSTGN CYVWNLTGGI GDEVTQLIPK TKIPAHTRYA120 LQCRFSPDST LLATCSADQT CKIWRTSNFS LMTELSIKSG NPGESSRGWM WGCAFSGDSQ180 YIVTASSDNL ARLWCVETGE IKREYGGHQK AVVCLAFNDS VLG 223

- (2) INFORMATION ON SEQ ID NO. 358:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

FFFFFFFF EQHLRVGLLL LPPRLSPRPG PAWPVPNPVG WPGHLHQGQ LLAGTNKPFH 60 LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLRPLSSFGP SADFPRQCRL AQSRSVQPGL120 GRALSHLDKQ LGAESPRAAW PSRSRRHRGP SGPVAQAGRG GSALTWVLHG SLQLPPPAPG180 SPEGSQASPA HCH

- (2) INFORMATION ON SEQ ID NO. 359:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 251 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

PGCCMGPSSC HHLHQAVPRG HRLAQHTVIE GQADNSLLVA AILSLDLSSL HTPEPGQVVR 60
GSSDDVLGVP REGAAPHPAA GGLPGVAALD AQLRHQGEVG RPPDLARLIS RAGGEERGVG120
AEATLQGVAR VGRDLSLGDE LGHLVTNAPR QIPDIAVSGA IDSCHVAGVG IDVGGRDGDL180
GLRDQLLVVV CFQVPDVDSP ALVTHDELCL GWGAAPGTPR VNALGGHTGP QHDCFLQVTS240
TSACMILTSS C 251

- (2) INFORMATION ON SEQ ID NO. 360:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360: GNIPHSNLTD ASSPKRIKIV ACTDQENILG RMKYVCLFFF KNKGFWNSGE

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- (2) INFORMATION ON SEQ ID NO. 361:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 59 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

KGNQLYQGET RALGTMTTRT AFILHHSDCF QSSNDCQATS QMTDNFCCSF LYKMLRQQA 59

- (2) INFORMATION ON SEQ ID NO. 362:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

DKILLSPRME CSGMIMAHCS LDLPGSHLSL PSSWDHRHVP PCPANFYFGR DKVSPCCLGR60 FQTPGLK

- (2) INFORMATION ON SEQ ID NO. 363:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 84 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

MRRCIHPSHS LSGSRQTQSP LSHSASNGST TKVAQQMRRA AAVVGESTEE TRLGRALGAA60 GFTNKQLSEN TAQGEEKRVM CLQN 84

- (2) INFORMATION ON SEQ ID NO. 364:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

CAYRTEKWKS HTVPCSPEVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDCLC 60 RGSTGQPTAN TAASLVSASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120 HHCIPNR 127

- (2) INFORMATION ON SEQ ID NO. 365:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A)	ORGANISM:	HUMAN
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

PYVHSPAWSP WGLVGRLVSV HTDIPATFRT LIVSAEVALG SQLQTQQPPW FQLLSFQYIL 60 ETTPGLIFLR TQHSLCHFSV RKPKMAPCHL EADQVITVSP TASTVCIWYI VQAP 114

- (2) INFORMATION ON SEQ ID NO. 366:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 30 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

NLHSNIKVFF YNVPKISGPQ QAVFVPVFFN

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- (2) INFORMATION ON SEQ ID NO. 367:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 44 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

KECMSEAQFL ATTLTKGNNC RGILQLIHTQ HLLHTVFTDS NLVG

44

- (2) INFORMATION ON SEQ ID NO. 368:
  - (i) SEQUENCE CHARACTERISTIC:

<ul><li>(A) LENGTH: 34 amino acids</li><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:	
NVDFRCKNML EIRFSAIKPN TKKIKKNVCQ KPNS 34	
(2) INFORMATION ON SEQ ID NO. 369:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 147 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:	
OPSSLIHHOP YPYPPRHLLA TPLLKPOLLA GSPAHASLIS FLASPORASR OHGGPSORAG 6	ia

(2) INFORMATION ON SEQ ID NO. 370:

EFRCPGSLGE WGEIPEKESS AHPKTEE

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 244 amino acids

TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPAA GDRRPLPEWG RVSLAESPGA120

- (B) TYPE: Protein (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

NHSCWQGPQL MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT 60 QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQK120 QKNDSDVTEV MWQPALRGR GLQAQGYGVR IQDAGVYLLY SQVLFQDVTF TMGQVVSREG180 QGRQETLFRC IRSMPSHPDR AYNSCYSAGV FHLHQGDILS VIIPRARAKL NLSPHGTFLG240 FVKL

- (2) INFORMATION ON SEQ ID NO. 371:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 185 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESFFCFWVS TALLFRDLSP LSQASRASEL 60 CSGRLCQGYP SPFWEGPPVP CSRLTSLLRL CSSVCWVSRA MAQATAPRAA PQLNQRATES120 AGSLTGPPML PGGPLGASKK GDEAGMSWGP CQQLWFQEWG SKEVAGRVRV RAVVQKGRRL180 LRKEK

- (2) INFORMATION ON SEQ ID NO. 372:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

VLYHCASRYR RRARQTCAPS YTRSADLPSR TPPVEDLLEL SRAFWVGADG GGRVRVLGGT 60 EAHEDGIPPE SMDHYADGHR PQHCHLGYRC HGRPQREGLP RCLKVPPVNL SSVSVPFPVT120 HRAGMEFNGC SGQTLVHGQT SLLWILQD

- (2) INFORMATION ON SEQ ID NO. 373:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 135 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CLPVRRLRQF EPKTPKVEAE FQSMGSRLSQ PFESYITAPP GTAAAPAKPA PPATPGAPTS 60 PAEHRLLKTC WSCRVLSGLG LMGAGGYVYW VARKPMKMGY PPSPWTITQM VIGLSIATWG120 IVVMADPKGK AYRVV 135

- (2) INFORMATION ON SEQ ID NO. 374:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 152 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

IPCLLCVSRG KGQRQKTDSL VVLSNNAVGL PFGVCHDNDT PGGNAEADDH LRNGPWTRGV 60 SHLHGLPCHP VHVPARPHQP QPRKHATAPA GLQQAVFCWG GRRSGCSWGR RFGGRGGTG120 RRSDIGLKRL GQPRPHALEL GLNLGRLWFK LA 152

(2) INFORMATION ON SEQ ID	NO.	375:
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- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GAELQLRSCA MAVSQEGLDG EVKAPDARIF IPCANTAFTP DLQVLQQVLS SFTVSSPLFH 60 SGFICYTPNL FSQSTPQSLP CWGQHRKRQN LRKEKGNLQP AMDLMIP 107

- (2) INFORMATION ON SEQ ID NO. 376:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

IPKNFYHNIH RSLYQLYLEV KQAWESIDCS ACPRVEALNK ATKTPEITDL TFQWPTGPGS 60 GQVGHQANHL FPCASLCKSW SVPLARPSLV QDLGPQTKES RGLGFPDPRM VSL 113

- (2) INFORMATION ON SEQ ID NO. 377:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

FGGPQAQPHS AVGSSLSSQI QVNLSFKNKG EPQTCSTTRD NNTPWQEDHV LDCLRTATVR 60 QEACCDPLCS MPIAQASSIP YHLPPMLFFG TTTLAKREYG KQRPRALLQY RHFEVGRQHM120 LHSK

- (2) INFORMATION ON SEQ ID NO. 378:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 66 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HKIILISRYR RNSVVTCQAI LYTPMILQRK HPSLLLPLLW QLKCICSSTL KRRKRNNLSL60 IPKLPH 66

- (2) INFORMATION ON SEQ ID NO. 379:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

PEKSPGAGPL LGGSPFFFFF YVSKSTEFIL KHSIKFESHE TKASLHYMLI LAKSKDQHTI60 DIHDNVV

- (2) INFORMATION ON SEQ ID NO. 380:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

FCIHFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNGDS FFRMLKAQCL RFMLAALLAL60 LLPEMKTKQN R 71

- (2) INFORMATION ON SEQ ID NO. 381:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

MDGAQGRLLP VSSRHSNLAL LKPTSRDLTA PPEGASLMTV GGITAPRDVQ VWNPRTWESV 60 TLRGKRDPAP VLQFRISWWG DDRGWLRWAL SNHGGPYKGR GVTRVCA 107

- (2) INFORMATION ON SEQ ID NO. 382:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 143 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

EVENHTNLLS YSSRGQESKM VFTRLKSCQC GFVSPRRLWG RIQCLFQLLQ GPPHRLAPGL 60 LAIFTARSFL ASCADPRDSP SLIRAPMITQ GPPQPSTVIS PPRNPELKHR RRVPFATQGN120 TFPRFGVPNL DISGGCYSTH RHQ 143

- (2) INFORMATION ON SEQ ID NO. 383:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

SHTHAQLSNH GGVQEPPLPL GVPKPWGSDS GALSRPGCKL KTPGGFQNAQ CLGHNLDQLN60 LNLQRDITAP QETPRGSQSA KPEETI 86

- (2) INFORMATION ON SEQ ID NO. 384:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

LEPIRFQQKV MEKETEKRIS EIEDAAFLAR EKAKQDAEYY AAHKYATSNK HKLTPEYLEL 60 KKYQAIASNS KIYFGSNIPN MFVDSSCALK YSDIRTGRES SLPSKEALEP SGENVIQNKE120 STG

- (2) INFORMATION ON SEQ ID NO. 385:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 83 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

DNSCVRYVEA QQKSHGTTSR NLSAVRPVSL MTVCWLCQTL YLGKESPDLN GSFPWALSYR60 GICNMEKIIF HFCSFNSINS LYK

- (2) INFORMATION ON SEQ ID NO. 386:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CLTFQCRQYL SIRLSSFMSS SLERNTYRIL DKTVAEKTIC VSDSWLYPPI SGAPRTIAGE60 VEQMKCKFSV NLKSPYNDCS HLTPWATS 88

- (2) INFORMATION ON SEQ ID NO. 387:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60 RDLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

- (2) INFORMATION ON SEQ ID NO. 388:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 173 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPPSSLFLP GAYKAQMYSD VWTNTKKKKK 60 KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAAFYQK120 GENSCLSFLK NAFLYLSIRH YTSELYKRPG GTMSLVDTFH CSVAPFLAWE ASA 173

- (2) INFORMATION ON SEQ ID NO. 389:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60 RDLLLLARLO GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

### (2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 262 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RCPRRGREMD SGCWLFGGEF EDSVFEERPE RRSGPPASYC AKLCEPQWFY EETESSDDVE 60
VLTLKKFKGD LAYRRQEYQK ALQEYSSISE KLSSTNFAMK RDVQEGQARC LAHLGRHMEA120
LEIAANLENK ATNTDHLTTV LYLQLAICSS LQNLEKTIFC LQKLISLHPF NPWNWGKLAE180
AYLNLGPALS AALASSQKQH SFTSSDKTIK SFFPHSGKDC LLCFPETLPE SSLIFCGRDT240
RNGRKIGKFC KCANLVGERG TG 262

- (2) INFORMATION ON SEQ ID NO. 391:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 66 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

KPVPLSPTRL AHLQNFPIFL PFLVSLPQKI KELSGKVSGK HKRQSFPECG KKDLIVLSLE60 VKLCCF

- (2) INFORMATION ON SEQ ID NO. 392:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

QAGGRVPWLN GLCWLLYFPS LQQSPAPPYA YPGEPDTEPD LPGHPFSWQN WLMTIFQRYW60 NTPAVLSDTL VVCRPGLL 78

- (2) INFORMATION ON SEQ ID NO. 393:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

TSLEGIDLOP SHLTIYTAAL KEKTPDFRRL SPRVSETADS RKVARGPRFV MRDNPGRGGD60 HRGLOAPGWM KEGRGWGVL 79

- (2) INFORMATION ON SEQ ID NO. 394:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 72 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

VTPPPPSQIS SFLPPSTAPF TKPPIPDPPS STPAPGDPYD HPRARGCPAL QIGAHGRPYG60 SPRSPRREER DV 72

- (2) INFORMATION ON SEQ ID NO. 395:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

PPPPPPKFHP SFRLLQPPLQ NPPSPTLLHP PRRLETPMIT PAPGVVPHYK SGPTGDLTGV60 RGLRDARRET SEVWRLFLQG CCVDCEVGGL KINSLEGG 98

- (2) INFORMATION ON SEQ ID NO. 396:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

NWRQTVWQRV REGACAQESS RPASGCRFLR CAIGASAFSG DRGSAVATNT QPHTHNHTHK60 WGQPHPVQAF TNVISVLFYF 80

- (2) INFORMATION ON SEQ ID NO. 397:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 309 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

YDNSSTCKKG KVFPGKISVT VSETFDPEK HSMAYQDLHS EITSLFKDVF GTSVYGQTVI 60
LTVSTSLSPR SEMRADDKFV NVTIVTILAE TTSDNEKTVT EKINKAIRSS SSNFLNYDLT120
LRCDYYGCNQ TADDCLNGLA CDCKSDLQRP NPQSPFCVAS SLKCPDACNA QHKQCLIKKS180
GGAPECACVP GYQEDANGNC QKCAFGYSGL DCKDKFQLIL TIVGTIAGIV ILSMIIALIV240
TARSNNKTKH IEEENLIDED FQNLKLRSTG FTNLGAEGSV FPKVRITASR DSQMQNPYSR300
HSSMPRPDY

- (2) INFORMATION ON SEQ ID NO. 398:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

QALIASTIFN VIDSYLASEL DSLQTFTTSI QRGWQMSDGR KTPEARSLLV LTSPSVFLNT 60 LNNSLYIGWG PWRVPHSYDS NSQGGACCCV LNRDFASGCL WRPLS 105

- (2) INFORMATION ON SEQ ID NO. 399:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

CFSCFVICSV SLCTLNIYPL CDKKKKKKK SRTSTFDFSQ PQPRKNGSWD KQLVFVSKTQ60 IGHINATAFR SFDFD 75

- (2) INFORMATION ON SEQ ID NO. 400:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

RKKAVCFMND LICFLDNTFK NNVLSQAWWC VHLVPTIWEA EAGGSLEPRS LKLQCPVVAP60 VNNCTPAWAT

- (2) INFORMATION ON SEQ ID NO. 401:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 69 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

LVPQGSLLQT HPFVFFSFLE MRSRYVAQAG VQLFTGATTG HCSFKLLGSS DPPASASQIV60

GTRCTHHHA

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- (2) INFORMATION ON SEQ ID NO. 402:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

PPLWVATVRN GCCHVFWTLP ANRSLPGFGN TSITSLLLFC RDKTFEVARP RTSKDSCYSAGO TVYTAHLSYS HVLSSLVRLF 80

- (2) INFORMATION ON SEQ ID NO. 403:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 81 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLLP RCYFSAGIKL LRWPDPEHPR60 IPVTVLQYTL LIYPILMCFL L 81

- (2) INFORMATION ON SEQ ID NO. 404:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

VSHYPHSVSK PPKHQTKQMV VALTHSRLTS EFKWENTPYT TVIIPLWTLN ITYFLKIILL60 KKKAHENRIN EQCIL 75

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 328 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

RYLNMGNLLK VLTCTDLEQG PNFFLDFENA QPTESEKEIY NQVNVVLKDA EGILEDLQSY 60 RGAGHEIREA IQHFADEKLQ EKAWGAVVPL VGKLKKFYEF SQRLEAALRG LLGALTSTPY120 SPTQHLEREQ ALAKQFAEIL HFTLRFDELK MTNPAIQNDF SYYRRTLSRM RINNVPAEGE180 NEVNNELANR MSLFYAEATP MLKTLSDATT KFVSENKNLP IENTTDCLST MASVCRVMLE240 TPEYRSRFTN EETVSFCLRV MVGVIILYDH VHPVGAFAKT SKIDMKGCIK VLKDQPPNSV300 EGLLNALRYT TKHLNDETTS KQIKSMLQ

- (2) INFORMATION ON SEQ ID NO. 406:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 115 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes.
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

YYIHLIINFL LRLCRLGIFK IKEKIWPLLK VCACQNFKKI PHVKVPSASA GDSVLVLLSS 60 ARASRRSQSR SCALLDRRGG SSAALGGAPG PERGSGGSRT GSPSTPAPVA EPPQA

- (2) INFORMATION ON SEQ ID NO. 407:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 100 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN .
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

QEPALALDAG WENMGYLLRL PEDLLMLLLT SEKIRKISLI CLLVEQLHPM PSLATSHLLD 60 AGLPLVFRGQ LLCMTASPPR CLLHLLILHS PDYKFPSQTL 100

- (2) INFORMATION ON SEQ ID NO. 408:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 116 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

TVLHSHLPSS CLPCLSTHSV KEPRGATSPR LCFPTACGMG VSSATAGLRC FHQPCRHLVL 60 HEEQTLRGWS GMGRSPLGGQ ALVPSRFPSL APGVHTAQSA PGGWKPPCFR SLGSPP 116

- (2) INFORMATION ON SEQ ID NO. 409:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

SPDERCSIRT SPPRACPASP RTVLRSQEEP LRPDFVSPPP AAWVCPVPPL ASAASISLVA 60 TWSFMKSRHL EAGREWGGRP WEGRRWFQAG SRPWRLECTQ PSRHLVAGSH PALDHSGPHL120 RRVPALDQSR GH

- (2) INFORMATION ON SEQ ID NO. 410:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

WKQRRPAVAL DTPMPQAVGK QSLGEVAPLG SLTLCVERQG RHEEGRCEWS TVHPGISQPE 60 SPPSLAAPEH SLWPTATEMS ACQDTWRRKK TRHQKKLPPQ EQIELLDQGH TRSGRHPAPC120 AQGKETQFNV WLLCSRETAT LP

- (2) INFORMATION ON SEQ ID NO. 411:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

KRRGVRQFRW LVCTRRASPG AARSAPIAPA TGSGRRPNMD SAGQDINLNS PNKGLLSDSM 60 TDVPVDTGVA ARTPAVEGLT EAEEEELRAE LTKVEEEIVT LRQVLAAKER HCGELKRRLG120 LSTLGELKQN LSRSWHDVQV SSAYVKTSEK LGEWNEKVTQ SDLYKKTQET LSQAGQKTSA180 ALSTVGSAIS RKLGDMRNSA TFKSFEDRVG TIKSKVVGDR ENGSDNLPSS AGSGDKPLSD240 PAPF

- (2) INFORMATION ON SEQ ID NO. 412:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 149 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

LGHFLIPLSK FLRSFHIGAR DLHVMPAPGQ VLFQLPQGGE AQPPLELSTV PLLGCQDLAQ 60 SDNFLFHLGK LSPELLLLSL CQTLNSRSPG SHTCVDRNIR HGVRQQTFVR RIQVDILAGG120 VHVRAASGPC RGRYGSRAGG AGRSSPRTH

- (2) INFORMATION ON SEQ ID NO. 413:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 143 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

ALETCTSCQL LDRFCFSSPR VERPSLLLSS PQCLSLAART WRRVTISSST LVSSALSSSS 60 SASVRPSTAG VRAATPVSTG TSVMESDSRP LLGEFRLISW PAESMFGRRP DPVAGAMGAE120 RAAPGEARRV HTSQRNCLTP RRF

- (2) INFORMATION ON SEQ ID NO. 414:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

RGRGALWWAA KELRRTKKLS DYVGKNEKTK IIAKIQQRGQ GAPAREPIIS SEEQKQLMLY 60 YHRRQEELKR LEENDDDAYL NSPWADNTAL KRHFHGVKDI KWRPR 105

- (2) INFORMATION ON SEQ ID NO. 415:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 386 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

AAELRDCGSR RISRSPSSNS HLSPRISLSG NLGPQTSRLG GPPSPSATWS VFWQLPRQQS 60
LPGRGSANLL PSVRSESAVL SDCVGGFPGR SSVRAWIAGP RCTPASPTRV LSLSWRLFNS120
ASLLLLATST SGSECRFPRS PRARERGIPD CERLLVRRSC WRSGDPRPAG PAGHAAGAFS180
TPQYLGGTAM VLLHVKRGDE SQFLLQAPGS TELEELTVQV ARVYNGRLKV QRLCSEMEEL240
AEHGIFLPPN MQGLTDDQIE ELKLKDEWGE KCVPSGGAVF KKDDIGRRNG QAPNEKMKQV300
LKKTIEEAKA IISKKQVEAG VCVTMEMVKD ALDQLRGAVM IVYPMGLPPY DPIRMEFENK360
EDLSGTQAGL NVIKEAEAHC GGQPRS

- (2) INFORMATION ON SEQ ID NO. 416:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GVEKAPAAWP AGPAGRGSPD RQQLRRTNSR SQSGIPRSLA RGERGKRHSL PEVDVAKSNS 60 EAELKSRQLK LRTRVGEAGV HRGPAIQART ELRPGKPPTQ SERTADSERT DGRRFADPLP120 GSDCCRGNCQ NTDQVAEGEG GPPNRLVWGP RFPLREIRGL RWELLDGERE IRREPQSRSS180 AA

- (2) INFORMATION ON SEQ ID NO. 417:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 467 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

HTLSRWTKHS IPRWNDARTD DTWHSELDMR KIGQARNTLM DMRLSQVSDS VSGQTVVDPK 60
GYLTDLNSMI PTHGGDINDI KKARLLLKSV RETNPHHPPA WIASARLEEV TGKLQVARNL120
IMKGTEMCPK SEDVWLEAAR LQPGDTAKAV VAQAVRHLPQ SVRIYIRAAE LETDIRAKKR180
VLRKALEHVP NSVRLWKAAV ELEEPEDARI MLSRAVECCP TSVELWLALA RLETYENARK240
VLNKARENIP TDRHIWITAA KLEEANGNTQ MVEKIIDRAI TSLRANGVEI NREQWIQDAE300
ECDRAGSVAT CQAVMRAVIG IGIEEEDRKH TWMEDADSCV AHNALECARA IYAYALQVFP360
SKKSVWLRAA YFEKNHGTRE SLEALLQRAV AHCPKAEVLW LMGAKSKWLA GDVPAARSIL420
ALAFQANPNS EEIWLAAVKL ESENDEYERA RRLLAKARTV PPPPGCS

- (2) INFORMATION ON SEQ ID NO. 418:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 352 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TPGRWGHCPR LGQQPPGPLV LIILGLQLHG CQPDLLTVGV GLEGQGQDAP CCRHIPCQPL 60 GLGAHEPQHL CFGAVGHSPL QECFQGLPSA MVLLEVRGAQ PHTLLAGEHL QGVGVDGSCT120 LQGIVGYTTV SILHPGMLPI FLLNPNPNHG THDGLAGGHT PSPVTFLGIL DPLLTVDLHT180 VGPQRGDGSV DDLLHHLRVP IGFLQLSSRD PDMSVCRNVL PRLVQDLAGI FIGLQPCQSK240 PELHAGGAAL HSSAQHDSSI FRFFQLNGCF PQANRVWNML EGFPKNPLLC TNVRFQLCGS300 DVNPDRLWEM TDSLGYHGLG CVPRLQPGCF QPDIFTLGAH LRPLHDKVPS YL 352

- (2) INFORMATION ON SEQ ID NO. 419:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 424 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

PPGAPFFLFF FFLTRDIKTF NEGGHSSEPF HMRPNPAPRR PAMATAQSEG VLDAAGHQPK 60
DVPDLLLPVG DVLGHGAPQL PMPRLCTLTA LPHLLLLLS AMLQLKLVEE GPGIPQVRVN120
LHSAVEPLPG LGDLPLTPKQ LGHGQEHMGV MLTLLQGIHA LGPPLGPCLE EDGLRPQDTG180
VGALLQRLGH ECICDVLQPR TVLQPHGLQP QPRVLWVLQT RLFQNGPCSS KLPNLLLQPR240
EQKPQGCGVG TLLQPLVIGF PRLLHHLLLL LDLPLHHPQL GEVLIVPQGL LAQILGCPDV300
VLHPLQLHRL HEHPGGGGTV RALASSLRAR SYSSFSDSSF TAASQISSLL GLAWKARAPM360
LLAAGTSPAS HLDLAPMSHS TSALGQWATA LCRSASRDSR VPWFFSKYAA RSHTLFLLGN420
TCRA

- (2) INFORMATION ON SEQ ID NO. 420:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 109 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GRTLPRGGGT VWVQGHGLEG WWAALSGSGF PAVGFLFWLL RLVYFLSLLP VTPGAPEYRL 60 FSPWAVSLSC FLTLLPGLLC VHLRLAWSKQ VRPLLLYSLV LFWHLVKLA 109

- (2) INFORMATION ON SEQ ID NO. 421:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 177 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

VSVPSSSAAG TLFQGLCGAP DAPHPLSKIP GGRGGGRDPS LSALIYKDEK LTVTQDLPVN 60 DGKPHIVHFQ YEVTEVKVSS WDAVLSSQSL FVEIPDGLLA DGSKEGLLAL LEFAEEKMKV120 NYVFICFRKG REDRAPLLKT FSFLGFEIVR PGHPCVPSRP DVMFMVYPLD QNLSDED 177

- (2) INFORMATION ON SEQ ID NO. 422:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

ASRPYILELR EKDPCRPLAH RGSSTVGEGH QEHHRGPGTM CLQHWSWGHL LNGKILLSWV 60 FIILGGSAQG GRRRGEWVG GRVGGCGVAR AGRSLWAKSL SGRGRVPSSC LSER 114

- (2) INFORMATION ON SEQ ID NO. 426:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

(vi)		0	RI	GIN	
	,	-		ODGANT CM.	

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

PFCSSLAKLQ GIWGMWDLQF PAPASALSQV LTPAPASAPA PGRAPAPAAA

50

## (2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 114 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

  EDKMRPGLSF LLALLFFLGQ AAGDLGDVGP PIPSPGFSSF PGVDSSSSFS SSSRSGSSSS 60

  RSLGSGGSVS QLFSNFTGSV DDRGTCQCSV SLPDNNFPVD RVERWNSQLI VISQ 114
- (2) INFORMATION ON SEQ ID NO. 428:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

EITMSCEFQR STLSTGKLLS GRETEHWQVP RSSTEPVKLE NNWDTEPPLP KLRLELEPDL 60 ELELKLELES TPGKELKPGL GIGGPTSPKS PAAWPRKNRR ARRNERPGLI LSS 113

- (2) INFORMATION ON SEQ ID NO. 429:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAAGAGARPG AGAEAGAGVN TWERAEAGAG NWRSHIPQIP CSLAKEEQKG

50

- (2) INFORMATION ON SEQ ID NO. 430:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 224 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

QTQKVVTSPP RITLHWLLPC AAHPPDLHKK GQENSGCAPA TAHSAPPGRS PPELRAGLQR 60 LARAVLPVSR FSAPQPPAAS FSGPRVAPSE ESGPGTSSNS GRLALPRLRS LCPLGVARPR120 CCRALARCCC SSSPRTAAWA RRAGSSSLAS PTSPTSAELQ AHPGQPAAVP RHRIPEHAAA180 QPAGPRDHEG GAGAGRRLDP AGHEAVPPGH QEVPVLALRP RLPR 224

- (2) INFORMATION ON SEQ ID NO. 431:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 408 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

PALLGLPFIG SSLAPPTLQI CIKKAKKTLA VPQQRLILLP RVGAPRSCAR ACSASPALSS 60 RCPASPRPSR RLPAFRGPES HPAKRAGPGQ ARTPAASPFP GSAPSAPSGS RAHDAAGPWL120 AAAALPRLAL LPGLGARALP LWPARLLQA QNCKPIPANL QLCHGIEYQN MRLPNLLGHE180 TMKEVLEQAG AWIPLVMKQC HPDTKKFLCS LFAPVCLDDL DETIQPCHSL CVQVKDRCAP240 VMSAFGFPWP DMLECDRFPQ DNDLCIPLAS SDHLLPATEE APKVCEACKN KNDDDNDIME300 TLCKNDFALK IKVKEITYIN RDTKIILETK SKTIYKLNGV SERDLKKSVL WLKDSLQCTC360 EEMNDINAPY LVMGQKQGGE LVITSVKRWQ KGQREFKRIS RSIRKLQC 408

- (2) INFORMATION ON SEQ ID NO. 432:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 323 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

VISFTFIFSA KSFLQSVSIM SLSSSFLFLQ ASHTFGASSV AGRRWSLLAR GMQRSLSWGK 60
RSHSSMSQQG KPKADMTGAQ RSFTCTQSEW HGWMVSSRSS RQTGAKSEHR NFLVSGWHCF120
MTSGIQAPAC SSTSFMVSWP SRLGSRMFWY SMPWHSCRLA GMGLQFCACR RSRAGQRGRA180
RAPSPGSSAR RGRAAAASQG PAASWARDPE GAEGAEPGKG EAAGVRACPG PALFAGCDSG240
PRKAGSRRLG RGEAGHREDS AGEALQARAQ LRGAPTRGSR MSRCWGTARV FLAFFMQIWR300
VGGAREEPMK GNPRRAGHYF LGL 323

- (2) INFORMATION ON SEQ ID NO. 433:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 333 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

RGRTWELFLA GRRVLVTGAG KGIGRGTVQA LHATGARVVA VSRTQADLDS LVRECPGIEP 60
VCVDLGDWEA TERALGSVGP VDLRGDCADM ELFLAGRRVL VTGAGKGIGR GTVQALHATG120
ARVVAVSRTQ ADLDSLVREC PGIEPVCVDL GDWEATERAL GSVGPVDLLV NNAAVALLQP180
FLEVTKEAFD RSFEVNLRAV IQVSQIVARG LIARGVPGAI VNVSSQCSQR AVTNHSVYCS240
TKGALDMLTK VMALELGPHK IRVNAVNPTV VMTSMGQATW SDPHKAKTML NRIPLGKFAE300
VEHVVNAILF LLSDRSGMTT GSTLPVEGGF WAC 3333

- (2) INFORMATION ON SEQ ID NO. 434:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 210 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

APGHNLRHLD DRTQVHLKGS VKGLLGDLQE GLQQGDSGVV HQQVHGAHAA QRPLGGLPVT 60 QVHAHGFYPR ALADKAVKIR LSPAHSHHPR ARRVQRLDRA APYTFACPGD QHPAAREEQL120 HVGAVSAQVH GAHAAQRPLG GLPVTQVHAH GFYPRALADK AVKIRLSPAH SHHPRARRVQ180 RLDRAAPYTF ACPGDQHPAA REEQLPCSPT 210

- (2) INFORMATION ON SEQ ID NO. 435:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

FFFFFFFFL GSRIRFIGGI GGRMSTAWGL RCVEGAQQAQ KPPSTGKVEP VVMPLRSLSR 60 KRMAFTTCST SANLPSGIRF SIVLALWGSL QVAWPMDVIT TVGFTAFTRI LWGPSSRAIT120 LVSMSRAPLV EQ

- (2) INFORMATION ON SEQ ID NO. 436:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

KAKSWYPSDF RFQELPENTR SQRVIFWSLF CRDSWEYGHP APRCGNESSR SGEAALADVQ60 LAAPVSNQLH PDGVEDRGVG GLLPELHHAE PYLV 94

- (2) INFORMATION ON SEQ ID NO. 437:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

FSGVCFAGIA GSMATLLHDA VMNPAEVVKQ RLQMYNSQHR SAISCIRTVW RTEGLGAFYR60 SYTTPSPISC 70

- (2) INFORMATION ON SEQ ID NO. 438:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60 LRSGVLRKFL EPKIRRNPGL SFLRSKMYYQ SAQVSTDS 98

- (2) INFORMATION ON SEQ ID NO. 439:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 270 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

RSVVRRCLKM AAEEPQQQKQ EPLGSDSEGV NCLAYDEAIM AQQDRIQQEI AVQNPLVSER 60
LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSHL EALLDDSKEL120
QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVSI240
QVEYMDRGEG GTTNPHIFPE GFRAQGLTLF 270

- (2) INFORMATION ON SEQ ID NO. 440:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 145 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

RWRRRNLSSR SRSRWAATPK VLTVWPMMKP SWLSRTEFSK RLLCRTLWCQ SGWSSRSYTR 60 SMLKMTTSIN RRSRTSTKST RTSARPGLTA TVSIGLSDSP TWRHCWMTAR SCSGSRLCLP120 RARKTWCPRA SLNSQLRIST TRSWT

- (2) INFORMATION ON SEQ ID NO. 441:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 210 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

IAPSRLKQGK TLGSEALRED VRIGGAALAA VHVLHLDGHA EGLGQRNDVD VVALLAHGLH 60 LLLAELLDSP STLDEVLEEL ALALQVARGE QPQVDHKVVG GALVIEGGQQ VGDRGLLHL120 LNQVHERVVE ILNCEFSEAL GHQVFLALGR HSLEPLQLLA VIQQCLQVGE SESPIETVAV180 RPGLADVRVL FVEVLDLLII DVVIFSILLV

- (2) INFORMATION ON SEQ ID NO. 442:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 322 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

NSERGRLQAM MTHLHVKSTE PKAAPQPLNL VSSVTLSKSA SEASPQSLPH TPTTPTAPLT 60
PVTQGPSVIT TTSMHTVGPI RRRYSDKYNV PISSADIAQN QEFYKNAEVR PPFTYASLIR120
QAILESPEKQ LTLNEIYNWF TRMFAYFRRN AATWKNAVRH NLSLHKCFVR VENVKGAVWT180
VDEVEFQKRR PQKISGNPSL IKNMQSSHAY CTPLNAALQA SMAENSIPLY TTASMGNPTL240
GNLASAIREE LNGAMEHTNS NESDSSPGRS PMQAVHPVHV KEEPLDPEEA EGPLSLVTTA300
NHSPDFDHDR DYEDEPVNED ME

- (2) INFORMATION ON SEQ ID NO. 443:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

FGTRAPASHD DPPACEVYRT QSCPSAPESG IKCHPLQVRI GGFSTELTSY SNDPNRPPDS 60 RHPRPLCHHN HQHAHGGTHP QAVLRQIQRA HFVSRYCAEP RIL 103

- (2) INFORMATION ON SEQ ID NO. 444:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

SLSWSKSGLW LAVVTKDRGP SASSGSRGSS LTCTGCTACI GDLPGLLSLS LLLVCSIAPF 60 SSSRIALAKL PRVGFPMEAV VYRGILFSAI EACKAALRGV Q 101

- (2) INFORMATION ON SEQ ID NO. 445:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 539 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

LDVQVKDDSR ALTLGALTLP LARLLTAPEL ILDQWFQLSS SGPNSRLYMK LVMRILYLDS 60
SEICFPTVPG CPGAWDVDSE NPQRGSSVDA PPRPCHTTPD SQFGTEHVLR IHVLEAQDLI120
AKDRFLGGLV KGKSDPYVKL KLAGRSFRSH VVREDLNPRW NEVFEVIVTS VPGQELEVEV180
FDKDLDKDDF LGRCKVRLTT VLNSGFLDEW LTLEDVPSGR LHLRLERLTP RPTAAELEEV240
LQVNSLIQTQ KSAELAAALL SIYMERAEDL PLRKGTKHLS PYATLTVGDS SHKTKTISQT300
SAPVWDESAS FLIRKPHTES LELQVRGEGT GVLGSLSLPL SELLVADQLC LDRWFTLSSG360
QGQVLLRAQL GILVSQHSGV EAHSHSYSHS SSSLSEEPEL SGGPPHITSS APELRQRLTH420
VDSPLEAPAG PLGQVKLTLW YYSEERKLVS IVHGCRSLRQ NGRDPPDPYV SLLLLPDKNR480
GTKRRTSQKK RTLSPEFNER FEWELPLDEA QRRKLDVSVK SNSSFMSRER DCWGRCSWT 539

- (2) INFORMATION ON SEQ ID NO. 446:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

LLCLPAFVSL HHRLNVMSLK LGSKGRACAL QPFHLTGPYS GLCLTKEKNR MFPLLHGLYP60 SGPLGRGPEL AVSCFACTLF SLPPNSSGPS VSVPGQWQH 99

- (2) INFORMATION ON SEQ ID NO. 447:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

	(XI) BEQUENCE BESCRIFTION. BLg IS NOT III.
VV SS	WIKLFTCST SSNSAAVGRG VRRSRRKCRR PDGTSSRVSH SSRKPLFKTV VRRTLHLPRK 60 SLSKSLSKT STSSSWPGTD VTITSKTSFQ RGLRSSRTTW LRKLRPANFS LT 112
(2) I	NFORMATION ON SEQ ID NO. 451:
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 56 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
	(ii) MOLECULE TYPE: ORF
	(iii) HYPOTHETICAL: yes
	(Vi) ORIGIN (A) ORGANISM: HUMAN
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:
FFFFFVE	TGF RHVDETGLEL LASSDLPPQL LKVLGLYRHE PLSLALKRFS QRPSVR 56
(2) I	NFORMATION ON SEQ ID NO. 452:
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 56 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
	(ii) MOLECULE TYPE: ORF
	(iii) HYPOTHETICAL: yes
	(vi) ORIGIN (A) ORGANISM: HUMAN
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:
IRFGÍS	SCPGP GISLQEPLPL CWRHSFRIRR RREKRKCKGG RSFPGRTISV THMDPR 56
(2) I	NFORMATION ON SEQ ID NO. 453:
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 57 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

VTEMVRPGKD LPPLHFLFSL LLLILKLCLQ QRGRGSCREI PGPGQEMPNL IYLTEGL 57

- (2) INFORMATION ON SEQ ID NO. 454:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

ILAFWRAAPL WHHQTLLCFP STWNSSNIRG CEGLAILLSW VHVSDRNGAA WERSPSFTFS60 LLPPPPYSKT VPPTEGQGLL 80

- (2) INFORMATION ON SEQ ID NO. 455:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

ARLPLLAAED RGQPGSVKDP KMAGRKLALK TIDWVAFAEI IPQNQKAIAS SLKSWNETLT 60 SRLAALPENP PAIDWAYYKA NVAKAGLVDD FEKKFNALKV PVPEDKYTAQ VDAEEKEDVK120 SCAEWVSLSK ARIVEYEKEM EKMKNLIPFD QMTIEDLNEA FPETKLDKKK YPYWPHQPIE180 NL

(2) INFORMATION ON SEQ ID NO. 456:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 76 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:
AQSIAGGFSG KAANLEVRVS FODFRELAMA FWFWGMISAK ATQSMVFRAS FRPAILGSFT60 DPGCPRSSAA SNGSRA 76
(2) INFORMATION ON SEQ ID NO. 457:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 104 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:
CPECVIQGPE LPPGLNFINS QLVGEANRDT FSCLIWFLGK LHSSPQWSSD QMELSSSSSP 6 SLSHILQSWP LRETPTQHKI SHLLFLRHPP GQYIYPLARE PSAH 10
(2) INFORMATION ON SEQ ID NO. 458:
(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 223 amino acids
  (B) TYPE: Protein
  (C) STRAND: individual
  (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

RGAGGHQGES GRPEGWPPPF LHPRGRFQVP WLESVLIVVS NNIDEEALAR LAQEGSEVNV 60 IGIGTSVVTC PQQPSLGGVY KLVAVGGQPR MKLTEDPEKQ TLPGSKAAFR LLGSDGSPLM120 DMLQLAEEPV PQAGQELRVW PPGAQEPCTV RPAQVEPLLR LCLQQGQLCE PLPSLAESRA180 LAQLSLSRLS PEHRRLRSPA QYQVVLSERL QALVNSLCAG QSP 223

- (2) INFORMATION ON SEQ ID NO. 459:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

VIRVVSSQPR SESQGDCPAH RLFTRACSLS DSTTWYCAGL RSRLCSGLSR LRDSWAKALD 60 SARDGSGSHS CPCWRQSRSS GSTWAGLTVQ GSWAPGGHTL SSCPACGTGS SANCSMSMSG120 DPSEPRSRKA ALLPGNVCFS GSSVSFIRGW PPTATSL 157

- (2) INFORMATION ON SEQ ID NO. 460:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 93 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

PPLFPHLLFL WGKVSDSCCF QSAPLRVSGG LPRTQTVHQG LQPLGQHHLV LCRAPQPPVL60 RAESAQGQLG QGSRLCQGWE RLTQLSLLEA EPQ 93

- (2) INFORMATION ON SEQ ID NO. 461:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 328 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

FSLILCKHSI GDRKNYASAK LSELLPEEVE AEVKAAAEIS MGTEVSEEDI CNILHLCTQV 60
IEISEYRTQL YEYLQNRMMA IAPNVTVMVG ELVGARLIAH AGSLLNLAKH AASTVQILGA120
EKALFRALKS RRDTPKYGLI YHASLVGQTS PKHKGKISRM LAAKTVLAIR YDAFGEDSSS180
AMGVENRAKL EARLRTLEDR GIRKISGTGK ALAKTEKYEH KSEVKTYDPS GDSTLPTCSK240
KRKIEQVDKE DEITEKKAKK AKIKVKVEEE EEEKVAEEEE TSVKKKKKRG KKKHIKEEPL300
SEEEPCTSTA IASPEKKKKK KKKRENED

- (2) INFORMATION ON SEQ ID NO. 462:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

YNRNSFLLIL VLSLFFLFLL FLWTSNCCAG TWFFLRKWFF LNVFLFTPFL LLLHRCFFFF 60 CHFFFFLFFN FNFNLGFFGF LFSNFILFIY LFYFAFFRTG WKCGVTRRIV SLHFTFVFIF120 FCFC 124

- (2) INFORMATION ON SEQ ID NO. 463:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

SSFSLFFFFF FFFSGLAIAV LVHGSSSESG SSLMCFFLPL FFFFFTDVSS SSATFSSSSS 60 STLTLILAFL AFFSVISSSL STCSILRFLE QVGSVESPEG S 101

- (2) INFORMATION ON SEQ ID NO. 464:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 427 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

GGSSRRHGGG YAAVALLVLL LLGPGGWCLA EPPRDSLREE LVITPLPSGD VAATFQFRTR 60 WDSELQREGV SHYRLFPKAL GQLISKYSLR ELHLSFTQGF WRTRYWGPPF LQAPSGAELW120 VWFQDTVTDV DKSWKELSNV LSGIFCASLN FIDSTNTVTP TASFKPLGLA NDTDHYFLRY180 AVLPREVVCT ENLTPWKKLL PCSSKAGLSV LLKADRLFHT SYHSQAVHIR PVCRNARCTS240 ISWELRQTLS VVFDAFITGQ GKKDWSLFRM FSRTLTEPCP LASESRVYVD ITTYNQDNET300 LEVHPPPTTT YQDVILGTRK TYAIYDLLDT AMINNSRNLN IQLKWKRPPE NEAPPVPFLH360 AQRYVSGYGL QKGELSTLLY NTHPYRAFPV LLLDTVPWYL RLLHPLPACP GPAATPPPGD420 ADSAAGQ

- (2) INFORMATION ON SEQ ID NO. 465:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

SPSILYGSCT CHSHKAFGGP DTGGHPSCRP HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60 SSAPLSTSST PPTQSLPLPP SNPWVWPMTL TTTFCAMLCC RGRWSAPKTS PPGRSSCPVV120 PRQASLCC 128

- (2) INFORMATION ON SEQ ID NO. 466:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF .
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

PQAWRRLCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFRGRSRH IPVPHALGFG 60 ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLLEDP ILGATLPAGP IRCRAVGLVP120 RHCH

- (2) INFORMATION ON SEQ ID NO. 467:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

FLHKTHNRAV ÉEAKEPFLCL CSRTERGPLA SVSLLVLPGL YQALRRGMET PHSGAWLGEG 60 EAAGVLWASR GYNLSSLGNV CPFVGSSPTR RGTQLYTGTI CVWSVL 106

- (2) INFORMATION ON SEQ ID NO. 468:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

ISTKQTTHRL SQCKVESPDV SDYCLQMDTR SPESSDYTLE KPKEPLPPPL PQARPQSGAF 60 PYPASRPGTV REEPAGSRWP EGLSQSYYRG IKRAPLLPPQ PCCESCAGIN LRNSPEAETG120 LMPWERSECE PMAPSLLGTN LPKYVKAEGD RDLAEGRKSF SSRN 164

- (2) INFORMATION ON SEQ ID NO. 469:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

EIRGRPPLFM PPLSCVDEFL QNRPHTDCPS VKLSPPTCRT TAYKWTHVPQ RAQIIPSRSP 60 KNPCRLPFPK PGPRVGRFHT PPQGLVQSGK NQQAHAGQRA SLSPTTEA 108

- (2) INFORMATION ON SEQ ID NO. 470:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 317 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

NMVDYYEVLG VQRHASPEDI KKAYRKLALK WHPDKNPENK EEAERKFKQV AEAYEVLSDA 60 KKRDIYDKYG KEGLNGGGG GSHFDSPFEF GFTFRNPDDV FREFFGGRDP FSFDFFEDPF120 EDFFGNRGP RGSRSRGTGS FFSAFSGFPS FGSGFSSFDT GFTSFGSLGH GGLTSFSSTS180 FGGSGMGNFK SISTSTKMVN GRKITTKRIV ENGQERVEVE EDGQLKSLTI NGVADDDALA240 EERMRRGQNA LPAQPAGLRP PKPPRPASLL RHAPHCLSEE EGEQDRPGAP GPWDPLGVRS300 RIERRWQEEE AEAERGV

- (2) INFORMATION ON SEQ ID NO. 471:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

SMPLVQLPSS FKLLSLLLL PLATFFQSCC GRRGGPRARV PQVGPARPPP QRDSEARVSA 60 ARQAGAASAG GGRQAGLAGR SGLSACAPQR GHRRRPHHLL LRTLTGHLLQ LLLFLDRSRQ120 FSL

- (2) INFORMATION ON SEQ ID NO. 472:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

KIRSNQCLWS NFLPPSNSSL CFCFFLLPPS FNPAADAEGV PGPGCPRSVL LALLLRETVR 60 RVSQQRGRPG RLRRAEAGRL GWQGVLASPH ALLSEGIVVG HTIYC 105

- (2) INFORMATION ON SEQ ID NO. 473:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 159 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

IVSERSLRSL WTAHWALPEM DSRIPYDDYP VVFLPAYENP PAWIPPHERV HHPDYNNELT 60 QFLPRTITLK KPPGAQLGFN IRGGKASQLG IFISKVIPDS DAHRAGLQEG DQVLAVNDVD120 FQDIEHSKAV EILKTAREIS MRVRFFPYNY HRQKERTVH

- (2) INFORMATION ON SEQ ID NO. 474:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

- (2) INFORMATION ON SEQ ID NO. 475:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

LGGLSSSDVK SQLSSRRLLQ CDGSGQKLGQ LIVVVRVVYP LMRRNPCWRI LIGRQENHRV60 VIIRNPAVHL GQGPVGSPQR PQTPLTDNSV WEPEADA 97

- (2) INFORMATION ON SEQ ID NO. 476:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 274 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

GHLWRPAGGR LPRHHDQVCR AAEPHRGGGL CGHQRRLPHR PRVQEGWGLC PHESLHQVPA 60 DRPWHEPGAG CAADCEDPHR RPGACEPGAP PAARAAGLGR GTRHGNGDIL SFEDANRAMQ120 TGVTGIMIAR GALLKPWLFT EIKEQRHWDI SSSERLDILR DFTNYGLEHW GSDTQGVEKT180 RRFLLEWLSF LCRYDPVGLL ERLPQRINER PPYYLGRDYL ETLMASQKAA DWIRISEMLL240 GPVPPTSPSC RSTRPTRTSS LRLSQGHPGA RRVQ

- (2) INFORMATION ON SEQ ID NO. 477:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 256 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

AGPAPVQPGP HTRCRCPRGH GSRGRSQAGK LWCPAGPRRP GTSTPPSSPV RTCGPLTDED 60 VVRLRPCEKK RLDIRGKLYL APLTTCGNLP FRRICKRFGA DVTCGEMAVC TNLLQGQMSE120 WALLKRHQCE DIFGVQLEGA FPDTMTKCAE LLSRTVEVDF VDINVGCPID LVYKKGGGCA180 LMNRSTKFQQ IVRGMNQVLD VPLTVKIRTG VQERVNLAHR LLPELRDWGV ALVTEMGTSC240 HLRMPTAPCR LVSPGS 256

- (2) INFORMATION ON SEQ ID NO. 478:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 165 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

NLLYSPRPRV PLGKPEATCT RWPCASARRR GGGHWPKEHL ADADPVGCLL AGHQRLQVVA 60 AQVVGRPLVD PLWEPLQQPH GIVPAQEGQP LEQKAPGLLH ALRVRAPVLQ AVVGEVPQDV120 QALGRRDVPV PLLLDLREEP RLEQGATGNH DPGDTSLHGA VGILK 165

- (2) INFORMATION ON SEQ ID NO. 479:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 262 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

GSPMSPARAM QTLFVPEHGD HGAGVCSDHH HRGGHVPAEP LQAVCTVLHQ PAQPGAEERR 60 CPVLRRMPVA SETQCQATES QSRSLTPRLG PPTAWPCALR PAERFPPLPA QCLLHVQLQT120 LFVPEHGDHG AGVCSDHHHR GGHVPAEPLQ AVCTVLHQPA QPGAEERRCP VLRRMPVALG180 EHSVRQRNPR AAGLRPASAH RPPGRAALRP AGALPPLPAH LSVPAARDRP AAHHLAVRRG240 GAPTLPGPLD LQGSGPRGGV GN

- (2) INFORMATION ON SEQ ID NO. 480:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 270 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

AAQCLLHVQC KRSLFQSMEI TELEFVQIII IVVVTCLLSH YKLSARSFIS RHSQGRRRED 60
ALSSEGCLWP RRHSVRQRNP RAAVLRPASA HRPPGRAPFA QRSVFHRCQP NVSCTCNCKR120
SLFQSMEITE LEFVQIIIIV VVTCLLSHYK LSARSFISRH SQGRRREDAL SSEGCLWPSE180
STVSGNGIPE PQVYAPPRPT DRLAVPPFAQ RERFHRFQPT YPYLQHEIDL PPTISLSDGE240
EPPPYOGPWT FKVRDPEEL EIERGLGAET 270

- (2) INFORMATION ON SEQ ID NO. 481:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

ATTSCLHGPS SAGTARGGGE KMPCPQKDAC GPRRAQCQAT ESQSRRSTPR LGPPTAWPCR 60 PSPSGSASTA SSPPIRTCST RSTCRPPSRC QTGRSPHPTR APGPSRFGTP RRSWKLNGDW120 VRRP

- (2) INFORMATION ON SEQ ID NO. 482:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

RVLVSPLSLS MWRWKVEKDT VSILKLLRFS ERGRHLNRQV GFSVLSALGI WREMGLLSLC60 TQEGHALKTV FVDQRRLYST GGIQMSLRGR EETWQADYI 99

- (2) INFORMATION ON SEQ ID NO. 483:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 104 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

VLEEEKKHGK QITSEPFELC FSFFPCLFSK IYLNLETQDI FLGNLLPMSE VASAASRQIP 60 GNPEPQNVIP PGSAWPDPVL SAGFTYQSHS SFSINTPKSS PNHH 104

- (2) INFORMATION ON SEQ ID NO. 484:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

KLDSTQCRPS LHTNMYVLLS ECHLLCTQCH DSKIKISVSN QNINQARNSW AQRGVRGLSY 60 TAVKQPTCSA HSQAESDWSC RQRGGGRVLC CPLLCMVSWV FQGGQLLSPN KTVNSLRTGP120 LPH

- (2) INFORMATION ON SEQ ID NO. 485:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 303 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

LGRKPSWVGG AGLEPSQGSG LSHHPAPQSD SAPTSPPIPG EPGPQREVDK WGGSLGRPES 60
SGHPGRTPAT CCHCAAVMAR SGSATPPARA PGAPPRSPPQ RLVQDVSGPL RELRPRLCHL120
RKGPQGYGFN LHSDKSRPGQ YIRSVDPGSP AARSGLRAQD RLIEVNGQNV EGLRHAEVVA180
SIKAREDEAR LLVVDPETDE HFKRLRVTPT EEHVEGPLPS PVTNGTSPAQ LNGGSACSSR240
SDLPGSDKDT EDGSAWKQDP FQESGLHLSP TAAEAKEKAR AMRVNKRAPQ MDWNRKREIF300
SNF

- (2) INFORMATION ON SEQ ID NO. 486:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 149 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

APRRPRPRR LEPCESTSAR HRWTGTGSVK SSATSEPLPA CLGTLGPLPH GPWASACPEL 60 PQPQWTGGWS CHCPEISPSP GEPPSCPCPP GTGGLWQQDR GRETQRCERE SETETERERE120 RHRERQRESE RARGSRGARA FAALPGPAD 149

- (2) INFORMATION ON SEQ ID NO. 487:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 217 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

FLGNGRTTLQ STEAGGARGR LRPKVRAGGV PGSRDRQEGA QKLLKISRFL FQSICGARLL 60 TRMARAFSLA SAAVGLRWRP LSWKGSCFQA LPSSVSLSEP GRSLRDEHAE PPLSWAGLVP120 LVTGDGRGPS TCSSVGVTRS RLKCSSVSGS TTSSRASSR ALMLATTSAW RSPSTFCPFT180 SMSRSWARRP ERAAGEPGST ERMYWPGRDL SLCRLNP

- (2) INFORMATION ON SEQ ID NO. 488:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 298 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

EIRAVGGGVC VDGMGTPGEG LGRCSHALIR GVPESLASGE GAGAGLPALD LAKAQREHGV 60 LGGKLRQRLG LQLLELPPEE SLPLGPLLGD TAVIQGDTAL ITRPWSPARR PEVDGVRKAL120 QDLGLRIVEI GDENATLDGT DVLFTGREFF VGLSKWTNHR GAEIVADTFR DFAVSTVPVS180 GPSHLRGLCG MGGPRTVVAG SSDAAQKAVR AMAVLTDHPY ASLTLPDDAA ADCLFLRPGL240 PGVPPFLLHR GGGDLPNSQE ALQKLSDVTL VPVSCSELEK AGAGLSSLCL VLSTRPHS 298

- (2) INFORMATION ON SEQ ID NO. 489:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 175 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

AGHRYQGDIR ELLQCLLAVG QIPTSTVQEE RGHTRQPRTK KETVSSCVIW EGQGGIWVIC 60 QHCHCPDSLL GSVAAACHNS ARSPHAAETA QVGGTRDWHS GDGEVPERVR HDLSSSVIGP120 FGEAYEKLPA GEENVSAIQR RVLVSYFHNS EPQVLQGFAD SIDLWPTSGA PGPRD

- (2) INFORMATION ON SEQ ID NO. 490:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 150 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

LGPCPLGSRP CRQAAVPAAM TPQVAVLAAV APVVASVYLP APRAPFELWP DPEREGQPPH 60 LPPTPGSLGL PGSGHGSSGP APPPASPSHP HRLPLQPLGF LSFLVSSPVS SGHPHSCRAV120 ISAGAPPPED RVGGEGSPRL QASGTGSSGF

- (2) INFORMATION ON SEQ ID NO. 491:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 89 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

FVKRTKQPRQ TLDAPCSALR LWGRCLLGEA VAQGVHCEAG PVDSAGGIHL ASGCLVSVYS60 DIAFCCHLSC GQRGVSWHEN IFFFKCGSF 89

- (2) INFORMATION ON SEQ ID NO. 492:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 63 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

LTHLLFEKCL LPSLGLITKF DHDHIVVSQS ALEIVSGLHE VAMGVWSTLK LYQSCTYFQT60 FLK 63

- (2) INFORMATION ON SEQ ID NO. 493:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

DGSRMLCHYI QKQDNLKLNG CPLQSQQVQP HSARPELQPL PKGIFPTAST PSKEHQGFVS60 VVLFFLQTID IYS

- (2) INFORMATION ON SEQ ID NO. 494:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 318 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

KCATFWSFPR RQGGLGIAIS EEDTLSGVII KSLTEHGVAA TDGRLKVGDQ ILAVDDEIVV 60 GYPIEKFISL LKTAKMTVKL TIHAENPDSQ AVPSAAGAAS GEKKNSSQSL MVPQSGSPEP120 ESIRNTSRSS TPAIFASDPA TCPIIPGCET TIEISKGRTG LGLSIVGGSD TLLGAIIHE180 VYEEGAACKD GRLWAGDQIL EVNGIDLRKA THDEAINVLR QTPQRVRLTL YRDEAPYKEE240 EVCDTLTIEL QKKPGKGLGL SIVGKRNDTG VFVSDIVKGG IADADGRLMQ GDQILMVNGE300 DVRNATQEAV AVWIKVFP

- (2) INFORMATION ON SEQ ID NO. 495:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 206 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

SAFAEMGSDH TQSSASKISQ DVDKEDEFGY SWKNIRERYG TLTGELHMIE LEKGHSGLGL 60 SLAGNKDRSR MSVFIVGIDP NGAAGKDGRL QIADELLEIN GQILYGRSHQ NASSIIKCAP120 SKVKIIFIRN KDAVNQMAVC PGNAVEPLPS NSENLQNKET EPTVTTSDAA VDLSSFKNVQ180 HSGASQGGRG VWVLLSAKKI HSVESS

- (2) INFORMATION ON SEQ ID NO. 496:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 119 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

TSWIIMAPSS VSEPPTMLRP SPVRPLEISM VVSQPGIMGQ VAGSEAKIAG VDDLLVFRMD 60 SGSGEPDCGT IRDWELFFFS PLAAPAAEGT AWESGFSAWM VSFTVIFAVF RRLINFSIG 119

- (2) INFORMATION ON SEQ ID NO. 497:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SAPSLTKCRS THVYPLSLIM FMSGGSSRST LRRMVPTPST TSLSPRSSSS TSKLLTQSGP60 SLPQPPASRP F

- (2) INFORMATION ON SEQ ID NO. 498:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

SRSPACGASE HGDGAMSLIC SISNEVPEHP CVSPVSNHVY ERRLIEKYIA ENGTDPINNQ 60 PLSEEQLIDI KVAHPIRPKP PSATSIPAIL KALQDEWDAV MLHSFTLRQS CRQPAKSCHT120 LCTSTMPPAV SLPVSPRKL

- (2) INFORMATION ON SEQ ID NO. 499:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 74 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
     (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

TTGRERGCRP CAGLFYCFLF LMKLDHCLQN PAQALLPIPF TVSLVRRAMT RQAASCWYRA60

CDSSWRVVCS SGAE

74 . .

- (2) INFORMATION ON SEQ ID NO. 500:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

FSFFNETRSL LTKPCTSPPA HPLHSSLGSA SPVSQELQQN GCGTATTTSI ERQEGRGAVG60 LVQGFFIVFF F

- (2) INFORMATION ON SEQ ID NO. 501:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 284 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

EARGLATRTR SGAAAHAGDR FTDADDVAIL TYVKENARSP SSVTGNALWK AMEKSSLTQH 60 SWQSLKDRYL KHLRGQEHKY LLGDAPVSPS SQKLKRKAEE DPEAADSGEP QNKRTPDLPE120 EEYVKEEIQE NEEAVKKMLV EATREFEEVV VDESPPDFEI HITMCDDDPP TPEEDSETQP180 DEEEEEEEEK VSQPEVGAAI KIIRQLMEKF NLDLSTVTQA FLKNSGELEA TSAFLASGQR240 ADGYPIWSRQ DDIDLQKDDE DTREALVKKF GAQNVARRIE FRKK 284

- (2) INFORMATION ON SEQ ID NO. 502:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

ETFSSSSSS SSGCVSESSS GVGGSSSHIV ICISKSGGLS STTTSSNSRV ASTSIFLTAS 60 SFSWISSFTY SSSGKSGVLL FCGSPLSAAS GSSSAFRLSF WEEGLTGASP SRYLCSWPRR120 CLR

- (2) INFORMATION ON SEQ ID NO. 503:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 175 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

VFLRCGWIII THSYMYFKIR RALIHHNLLK LPGGFHKHLF OCFFILLDFF LHILFFRQIW 60 SSLILWFPAI RGLRVLLRLP LELLGGGAHR RVPQQVLMLL APQVLEVAVL QGLPRVLRER120 ALLHRFPQGV TGDGAGRAGI FLHVGKDGYV VRIREAIARV RCRSAPRARR QAPGF 175

- (2) INFORMATION ON SEQ ID NO. 504:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

CPPEKSLQMF QPLSSPDSHR KGTGFGLGIV FSLTFFKRRM WPLAFGSGMG LGMAYSNCQH60 DFQAPYLLHG KYVKEQEQ 78

- (2) INFORMATION ON SEQ ID NO. 505:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

SKTSTLPVAI WTRQRLEHLQ GFLGWTSITR ILSSRPHPPD TGPTSCRAPT QTCSPPAPPA60 FLSAGPRAPT PESLARAGNK SQVRKAGADA PDIAR 95

- (2) INFORMATION ON SEQ ID NO. 506:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 156 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

AIPNPMPEPK ANGHILLKK VSEKTIPNPK PVPFLWLSGL DRGWNICRDF SGGHQLPGFY 60 LHDRIRQTPV PLPAELRLRH VPHPRLQLSS RPAPALRPLK VSRELETSPR SGRQAQTLQI120 SRDDPLLPSL PVFSVGRQGD AVVWRLEVTL TLGCAY

- (2) INFORMATION ON SEQ ID NO. 507:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 169 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEOUENCE DESCRIPTION: SEO ID NO: 507:

AASGMLGSWP ARTFHPGACV SRRPSAPWKH TASGKDSPDL RFSEHGVSQE FWAGGLVAVL 60 EMTPSPSPWG TQEGPAGMCS LWVVGWCPCR GAGVRDLVLV HAGVWCKHVC AVQRDACGES120 RTPAPPRKGG AVTSVLCLFL IKTFPLFSYK FASCKQVHKD PPLVKSGFE 169

- (2) INFORMATION ON SEQ ID NO. 508:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 155 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TQNTGNRSAF PGWRWCAALS TRVSLYSTYM FTPHTCVDEH QITHPSSTTG TPADYPQAAH 60 SGRALLGAPR GGARGHLQHC HQAASPEFLG NTVLGKPKVR AVLPRGRVLP GCGGPAADTG120 PRVEGPGRPA SKHARRSLGE PGSVASSLLS LRSPI

- (2) INFORMATION ON SEQ ID NO. 509:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

ENRGNVLIKN KHKTLVTAPP FLGGAGVRLS PHASLCTAHT CLHHTPAWTS TRSRTPAPRQ 60 GHQPTTHRLH IPAGPSWVPH GEGLGVISST ATRPPAQNSW ETPCSENRRS GLSFPEAVCF120 QGAEGRRLTQ APGWKVLAGQ LPSMPDAA 148

- (2) INFORMATION ON SEQ ID NO. 510:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

NAYISGYERD FMTIQSNITL ADRETEVEND LPSLPASLRQ NWIPTLVFFL PFTSFSLLYN60 VLRDQNSHQN RLFLR 75

- (2) INFORMATION ON SEQ ID NO. 511:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

FRDTEGLLAL MTFWMGLQLM TILILEERTL LIFSPIALLR RSTSYSESLH IPLVFLQAPE60 PLVQMLY 67

- (2) INFORMATION ON SEQ ID NO. 512:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

IFFFFFFFF PLRHLFNNCR NPKELASNLE VVSEAAGWLD WAQPLSCLNR PRNGIMMTMR 60 TSILSSSHCV YYVFSFNKAF VPMALELGGR LKECVVILSK M 101

- (2) INFORMATION ON SEQ ID NO. 513:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 179 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

FGTMGGISDP DTLHIWKTNS LPLRFWVNIL KNPQFVFDID KTDHIDACLS VIAQAFIDAC 60 SISDLQLGKD SPTNKLLYAK EIPEYRKIVQ RYYKQIQDMT PLSEQEMNAH LAEESRKYQN120

EFNTNVAMAE IYKYAKRYRP QIMAALEANP TARRTQLQHK FEQVVALMED NIYECYSEA 179

- (2) INFORMATION ON SEQ ID NO. 514:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 179 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

DRGAPALTPG HLHPLPPVPR SVSGMEAREL VRLPHLPSTA CTVPTHLLHN VQLVLLPRAP 60 CIQAAKHKLG ERRPPARRLQ PRNSTSSTLV QGALLELTFD WFLLQLPKCY LHFPLTRRGS120 WPQTVSSSVR FLLLGRLLVE WAVPAPWGAL WASPGAGRVE GRDGGHRSWE PRLQEKERG 179

- (2) INFORMATION ON SEQ ID NO. 515:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 200 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

SGDRWEGMEV PRGQGGGAPV SESSPSSCPR PSRLCSVFPS LSHRHGVEDQ VEAQWASISP 60
SSSLTNSPCV SGLTVALVDV VLHQSHHLLK LVLQLCPPGR GVGLQRGHDL RPIPLGVLIN120
LCHGHIGVEL ILVFPRLLGQ MGIHLLLAER RHVLDLLVVA LHDLPVLRNL LGVEELVGWR180
ILAQLQVRDG AGVDEGLRDD 200

- (2) INFORMATION ON SEQ ID NO. 516:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

TSMEALLFRL FKLPATTLRC IGLRRPLVTH TLRRKCEHKA SRLCHGGCCC TLEPCVGRHR 60
DWDLERGKSS AKTGGELHGR RTAAARGGSE RPVLGHRRRD PDAGGLRGQD GEALQHRGWH120
IPGSETLPGR GGHVPWPRPG RRHPHHMCGF WDSQSLA 157

- (2) INFORMATION ON SEQ ID NO. 517:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 401 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

RTRCAGSVNT KPPGFVMAAA AARWNHVWVG TETGILKGVN LQRKQAANFT AGGQPRREEA 60 VSALCWGTGG ETQMLVGCAD RTVKHFSTED GIFQGQRHCP GGEGMFRGLA QADGTLITCV120 DSGILRVWHD KDKDTSSDPL LELRVGPGVC RMRQDPAHPH VVATGGKENA LKIWDLQGSE180 EPVFRAKNVR NDWLDLRVPI WDQDIQFLPG SQKLVTCTGY HQVRVYDPAS PQRRPVLETT240 YGEYPLTAMT LTPGGNSVIV GNTHGQLAEI DLRQGRLLGC LKGLAGSVRG LQCHPSKPLL300 ASCGLDRVLR IHRIQNPRGL EHKVYLKSQL NCLLLSGRDN WEDEPQEPQE PNKVPLEDTE360 TDELWASLEA AAKRKLSGLE QPQGALQTRR RKKKRPGSTS P

- (2) INFORMATION ON SEQ ID NO. 518:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 222 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

SWEKLYVLVP DGNPQVQPVI PHVLGPEHRF LRALQVPYLQ SILFPTCGNH MGVCWVLAHP 60 THPRAHSQFQ EWVRGCVLVL VMPDSENPRI HTCDEGAVGL GEATEHALPA RAVSLTLEYA120 ILGAEVLHRP VRAAHQHLGL AAGAPTQGAH CLLAPRLSSG REVRRLFSLK IYPFQDPSLG180 ADPHMVPACS SSRHDKAWRL CVHTSGAACA SPAGVEVRCT AV 222

- (2) INFORMATION ON SEQ ID NO. 519:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

DPRPVSLLTL ALLPRCHFLS SSVKYRLHIL SLNASTICVT PKDFWDFDET CEGEDTEKPV60 ICKHLLLFPH HLWDISAVVS KWQIIN 86

- (2) INFORMATION ON SEQ ID NO. 520:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 77 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

ISSVNYHMTI QAQYKLGHCI LCGWISVAVF LTSPKKTSCR AELLVQAPDN DAPDFAFWGL60 SLLLSHFLKL FAWPWHH 77

- (2) INFORMATION ON SEQ ID NO. 521:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

CGNKSKCLQI TGFSVSSPSQ VSSKSQKSLG VTQIVLALSD KMCSLYLTEE ERKWHLGSSA60 RVSKETGLGS Q 71

- (2) INFORMATION ON SEQ ID NO. 528:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

LTYLFFFFFF FFLGRSLGFT RSYGTLFRSE APPSHGYGDS GGRGNPSERP GGCWYSMYFR SC LPHLFHGVPC QGQALICGEG SKQRRRPFRG GERAVAPRTP SPAHDIPEKE TKIKPRGLST120

- (2) INFORMATION ON SEQ ID NO. 529:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 90 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

PLLKGKKLSA ALTNLSFFFF FFFFFGKKPW LYSLCGDTVP FRGPSQPWGG GQWWAWESQR60 ASWRVRRLHV FCSSPSFPWG PLPGSSTNMW 90

- (2) INFORMATION ON SEQ ID NO. 530:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

NKAPGPFYVG APLKYGMVVG REAVAQQSLS PDYQLWGGFQ GARSRLGSSS HRHVGGGRKY60 LQGGTVSEEQ DGRGFSACYG ILFKEMGVKP GTVAHA 96

## (2) INFORMATION ON SEQ ID NO. 531:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 497 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

TPALVQRFRE GGSGAPEQAE CVELLLALGE PAEELCEEFL AHARGRLEKE LRNLEAELGP 60
SPPAPDVLEF TDHGGSGFVG GLCQVAAAYQ ELFAAQGPAG AEKLAAFARQ LGSRYFALVE120
RRLAQEQGGG DNSLLVRALD RFHRRLRAPG ALLAAAGLAD AATEIVERVA RERLGHHLQG180
LRAAFLGCLT DVRQALAAPR VAGKEGPGLA ELLANVASSI LSHIKASLAA VHLFTAKEVS240
FSNKPYFRGE FCSQGVREGL IVGFVHSMCQ TAQSFCDSPG EKGGATPPAL LLLLSRLCLD300
YETATISYIL TLTDEQFLVQ DQFPVTPVST LCAEARETAR RLLTHYVKVQ GLVISQMLRK360
SVETRDWLST LEPRNVRAVM KRVVEDTTAI DVQVGLLYEE GVRKAQSSDS SKRTFSVYSS420
SRQQGRYAPS YTPSAPMDTN LLSNIQKLFS ERIDVFSPVE FNKVSVLTGI IKISLKTLAG480
SVCGLRTFLA LCGLQQG

## (2) INFORMATION ON SEQ ID NO. 532:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

CGSGWSWPHW PATRPGQGPP SQPREVLPAP GGRLSGSPGR PPGDPAGGGP GARGPLVPRS 60 PWQRLRARQR PAGPREPASA GGSGPAPAPA VSCHHHPAPA PAAAPPAQNS GCPAAGRRPP120 ASRHLLGPGP QTAPGRPPPP GRGRPRSHCL HGR

(2)	INFORMATION	ON	SEQ	ID	NO.	533:
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- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 221 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

YDQALHLHVV GQQPPRRFPG LCTQRAHGRH WELILHQKLF ISESEDVGDG GRLVVQAEAG 60 EQQEQGRWCG TPLLPRAVAE ALSRLAHRVD EAHDEALTDT LTAELTPEVG LVGEGHLFGG120 EKVHCCQRGL NVAQDGAGHI GQQLGQARAL LPSHARCCQR LADVCQAAQE GRPETLQVVA180 QALAGHSFHD LRGSVCEPGS GQQGPGSPQA PVEAVQRPHQ Q 221

- (2) INFORMATION ON SEQ ID NO. 534:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 52 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

PSILIPMTPG GFFSVMVRAK TGSTHRCSPA VYPLMRRIPC WRILIGRQET TG

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- (2) INFORMATION ON SEQ ID NO. 535:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 38 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

MOLECULE TYPE: ORF (ii) (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535: AGKKPPASHH KESGCPSRPS PTGHSTPPSD PLTDNSVW 38 (2) INFORMATION ON SEQ ID NO. 536: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 55 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes ORIGIN (vi) (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536: SGCVPSHEED SMLEDSHRQA RNHRLVIIRN PVVHLGQAPL ATPHRPQIRS LTIQS (2) INFORMATION ON SEQ ID NO. 537: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 113 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear MOLECULE TYPE: ORF (ii) (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

TRGPRKRLRR SGRRGGLRSW AGRERVLGTA LLGIYIVFPR IPGSGSEEAV TPYDRRDLDS 60

RNSPQAPAGQ STTSSSFCFC DGLESRGLKH TVSIDCIRFV QKPGQLTESH FLA

- (2) INFORMATION ON SEQ ID NO. 538:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

EPADSQARGR QCLLLLHQVQ GIWLKACIFP GHKLPEPLKW EARQFQTNLF STHHSTFKVC 60 LLLLPVHPPS LQFFHSLTSE RVPGGSMVNK LTCMLQKKKK K 101

- (2) INFORMATION ON SEQ ID NO. 539:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 198 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

YSLCSQCVSA PLTLNRHRSR RKRKWWIAQL EPGDCYDCLD LCGHRASQPP QTLSLECGGT 60 QCRFPGGLSP RPSPCPPSSS GLLFYRFFLV SFLGLLFTEG TAALGFLVTS ALLGSDGSAS120 ASWDLGMGTM MASTQMSWKM APRKSPYRSR FSRKVGSGTS GGEKSRSEAM AQVACCLTSL180 LTHHSLEPTP APPRRSPR

- (2) INFORMATION ON SEQ ID NO. 540:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

KKNSSALIFL EEAADFGCQI SLRNGHFLRC FFLTESVDKL IKRLSHFKIT PKSSSTVFFF 60 FSFCFKITNQ VRSPTSSSMN SFVTELLSVC SPHCALNTVS AAPVCPLFRK ESIFNTFTIC120 TPWNLHMLTS YYKPTHPQLS SGTGHPL

- (2) INFORMATION ON SEQ ID NO. 541:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

KNDRFPWTSL PGLKGALIKL FTEHVAEKHI YGLMPLLLEA QSTPFQVTPS TMANIVKGLY 60 TLRPEWVQMA PTLFSKFIPN ILPPAVESEL SEYAAQDQKF QRELIQNGFT RGDQSRKRAG120 DELAYNSSSA CASSRGYR 138

- (2) INFORMATION ON SEQ ID NO. 542:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 179 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

KACIPSDQSG FRWLQLYFLN LFQTFSLRRW NLNFLNMLLK IRNFKENLYR MVLQGVTSPG 60 RELGMSWLII ARQHVQVPGG TDSECIEYAF LPEKRTHWSC RDCIQSTVGA AHTQELCHKA120 VHGRGCWTS: LVCNFKTKTK KKKNSAARLG GDFEMGQSFW EFITRFCZEK ASQKVTISK 179

- (2) INFORMATION ON SEQ ID NO. 543:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 92 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

IQFLEAAFAV FLHCMRFGNE CRNLLWAFTF LCQFGFYCLN LMLTWRGDGG QCCCGASSES60 VCGELCCADV AVGGQVRGSA PSWKKSCLRV YV 92

- (2) INFORMATION ON SEQ ID NO. 544:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

KPNWHRKVNA HSKFLHSFPN RIQCKKTAKA ASRNCIYWPL PEQQAAMPAP WPPELDACCA60 DVLTLMRMLG YGSDSEEIHL SYSSLERSSC VFNMKHFIW 99

- (2) INFORMATION ON SEQ ID NO. 545:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

QSQNTKVFVP IRIYTDPLTK VLLIMQFASS PSSWLGSSPI WHDHIKRTPS DMISSKKVPS60 LLPDHQRPHQ HNTTLRIQIH CWPHNSTVPH LLSRSA 96

- (2) INFORMATION ON SEQ ID NO. 546:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GRDAGQSEPW LSTSGCCAWG GCAPGARGCW GPGPPSLGVG RKPGCRVSAS SVPERWIAWS 60 PRPSEASATF RGAPKSILTA RLWASAWRPQ HRGSQNERPW SSSMKTSG 108

- (2) INFORMATION ON SEQ ID NO. 547:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

PGRRAKRAMA VYVGMLRLGR LCAGSSGVLG ARAALSRSWQ EARLQGVRFL SSREVDRMVS 60 TPIGGLSYVQ GCTKKHLNSK TVGQCLETTA QRVPEREALV VLHEDVRLTF AQLKEEW 117

- (2) INFORMATION ON SEQ ID NO. 548:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

PLLLELGKGQ PDVFMEDDQG LSFWDPLCCG LQALAHSLAV KMLFGAPLNV AEASDGRGDH 60 AIHLSGTEEA DTLQPGFLPT PREGGPGPQH PRAPGAQPPQ AQHPDVDSHG SLCPASR 117

- (2) INFORMATION ON SEQ ID NO. 549:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

RLSGPAANPR GAAGWRAAGA QELGMSYKPM RPWLPSSTPW SARHPLGPGA PRFPDREACA60 CAVRGCSV 68

- (2) INFORMATION ON SEQ ID NO. 550:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GHCSPARRTR TPPCQGTGVP RAPGGAWQTR GCCWAARGAW VCRTSPTPGR QRHASRPLLG60 GWLRGRSA

- (2) INFORMATION ON SEQ ID NO. 551:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

DTAAPHGARA RLPVREPGCP GPQGVPGRPG GAAGQPGAHG FVGHPQLLGA SGTPAGRSSG60 VGCGAAQP 68

- (2) INFORMATION ON SEQ ID NO. 552:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 32 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:	
SPISITETQQ FSNNLIHTIT CLLRMALYLF SL	32
(2) INFORMATION ON SEQ ID NO. 553:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 33 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:	
ITLQPISQNM FLLLNNTQLF YLCVLFMPDH QYQ	33
(2) INFORMATION ON SEQ ID NO. 554:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 43 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(Vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:	

- (2) INFORMATION ON SEQ ID NO. 555:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

CFTHWNVFPR LWMTSFLMER VQEGWKTPGF KLSIPHMGFS IIFRPEAARP EVRLHLSALF60 VLLLATLGFL LGTMCGCGMC EQKGG 85

- (2) INFORMATION ON SEQ ID NO. 556:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

FNDGKTWQLK KTLVTNGGFL LFFPHPPFCS HMPQPHMVPS RNPKVARSST KRADKCRRTS 60 GRAASGLKMI EKPMWGMLSL NPGVFHPSWT LSIRKEVIHN RGKTFQ 106

- (2) INFORMATION ON SEQ ID NO. 557:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 109 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:	
NINYIEIIFL FLLLISPLGP HRLSPAQLAQ LAQLAHSPQV SRRHRALTMV SSHHPHPHSP SQRPLVVGPA VFQKGLTCTN LRQTYAPFSV SLASPSWED	GWHGVSNVAN 60 109
(2) INFORMATION ON SEQ ID NO. 558:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 50 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:	
LGIFVAYRNQ LGVPSLMRCS WKAIYARGGF TFVAPPFIDP SAFKKLECEN	50
(2) INFORMATION ON SEQ ID NO. 559:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 44 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

(vi) ORIGIN
(A) ORGANISM: HUMAN

(2)	INFORMATION ON SEQ ID NO. 560:	
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 45 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: ORF	
	(iii) HYPOTHETICAL: yes	
	(vi) ORIGIN (A) ORGANISM: HUMAN	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:	
RVNE	EWRSDKS ETTSCINGFP AASHKRRYTK LVPVSYKNAK LRMGV 45	:
(2)	INFORMATION ON SEQ ID NO. 561:	
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 34 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: ORF	
	(iii) HYPOTHETICAL: yes	
	(vi) ORIGIN (A) ORGANISM: HUMAN	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:	
M	RSRLPCEGL VARHPRELRV PSVRFWIDWP WVLT	.34
(2)	INFORMATION ON SEQ ID NO. 562:	
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 67 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

VSTHGQSIQK RTEGTRSSRG CRATSPSHGN RLLIQESFPQ NPPRARFQGH PLGRQSRQQP60 FTEAMSQ 67

- (2) INFORMATION ON SEQ ID NO. 563:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN.
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

APMASQSRSA LRARVAHAGA VPPALHTAID SSFRNHFLKT HQGLGSKGTR

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- (2) INFORMATION ON SEQ ID NO. 564:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 54 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

(2) INFORMATION ON SEQ ID NO. 565: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 57 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565: CTMVNVDNTV SFLSSFLNVN LYLTQSVCLK LLRTFPNVTG PFPFVIRGIL FQDYCCV 57 (2) INFORMATION ON SEQ ID NO. 566: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 49 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566: EKCQPHSLIL LWPFNFILIK SHRSHTTIIL KQNSSDYKGK WASNVGKCP 49 (2) INFORMATION ON SEQ ID NO. 567: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 94 amino acids (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567: GEGRVWNPEG SKSRHWPDHP APWAPSPRQE QLFSIPSQTS SIFITMTFRE VSQASSRCPT60

IPSGGKRQEN SPRVPVMLLS PSQFRLSRTS YLQP

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- (2) INFORMATION ON SEQ ID NO. 568:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

GLTLKKGTFP RGPEIQADPN LTPCSRTQAH RPLNSNPTSP PPPPTPDFLI SWNAFQDWKS60 POGSSEPILS PARISSMHPG HAFHISRNK

- (2) INFORMATION ON SEQ ID NO. 569:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - MOLECULE TYPE: ORF (ii)
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

DVLDSLNWDG ESSMTGTRGE FSCLFPPEGI VGHLELAWET SLKVIVIKIE LVWEGMENSC60 SCLGLGAQGA GWSGQCLDLL PSGFHTRPS

- (2) INFORMATION ON SEQ ID NO. 570:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

KSIAHSVIGY FHDFKWFYEE TESSDDVEVL TLKKFKGDLA YRRQEYQVEF NIWCLKWALV60 LSVMAYVNNS VPS 73

- (2) INFORMATION ON SEQ ID NO. 571:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 40 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

SADSQEIQRR PGLQTTRVSG RIQHMVLEVG SCFISYGICK

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- (2) INFORMATION ON SEQ ID NO. 572:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 60 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

NKSPLQAPYV EFYLILLSSV GQVSFEFLES QHFNIITAFC FFIKPLEIMK IAYYRVSYAF60

- (2) INFORMATION ON SEQ ID NO. 573:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 318 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GNLSLESLCN LYNWRYKNLG NLPHVQLLPE FSTANAGLLY DFQLINVEDF QGVGESEPNP 60
YFYQNLGEAE YVVALFMYMC LLGYPADKIS ILTTYNGQKH LIRDIINRRC GNNPLIGRPN120
KVTTVDRFQG QQNDYILLSL VRTRAVGHLR DVRRLVVAMS RARLGLYIFA RVSLFQNCFE180
LTPAFSQLTA RPLHLHIPT EPFPTTRKNG ERPSHEVQII KNMPQMANFV YNMYMHLIQT240
THHYHQTLLQ LPPAMVEEGE EVQNQETELE TEEEAMTVQA DIIPSPTDTS CRQETPAFER300
ESRPGGEGAI ALGGLGCF

- (2) INFORMATION ON SEQ ID NO. 574:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

KTPKPPQRNC PFPTGAALTL KGWSFLTAAG VCWTGYDVSL NSHGLFFCFO LCFLILNFLT60

- (2) INFORMATION ON SEQ ID NO. 575:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 155 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

SLMIMMCSLY QMHVHVVYKV CHLGHIFYYL YFMRWSLSIL SSSWERFCWN YMQMKGASCE 60 LTESWSQFKT VLEEGYSGED IKSKSGSRHG HYQATDIPQM AHCPGSYQRK KNIVILLTLK120 SINSCHLVWS SNOWIVSTSS IDDVANKMLL AIICC

- (2) INFORMATION ON SEQ ID NO. 576:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - MOLECULE TYPE: ORF (ii)
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

DHLGFISTKM RTNHGVRKGS LEEHKNLKAL GGYHYYISYF HRSDLAKLCI LSLLTFI

- (2) INFORMATION ON SEQ ID NO. 577:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 48 amino acids
    - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCF DESCRIPTION: SEQ ID NO: 577:
CSF CCILCKKTAN RGKRTLQIKT ILVSFPQR
(2) INFORMATION ON SEQ ID NO. 578:
<ul><li>(i) SEQUENCE CHARACTERISTIC:</li><li>(A) LENGTH: 48 amino acids</li><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li><li>(D) TOPOLOGY: linear</li></ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:
LYFFKTLKEK CVLFAASFVR RLPTEEKGLY KLRPSWFHFH KDENKSWC
(2) INFORMATION ON SEQ ID NO. 579:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 48 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

GSFPNTMICS HLCGNETKMV LICKVLFPLL AVFLQRMQQK EHIFLSKF

48

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- (2) INFORMATION ON SEQ ID NO. 580:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 48 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

HCRILQGLSP LVGREKTTQV MRNFYSFQEL EEQLLIKFHA LVTKYFYS

48

- (2) INFORMATION ON SEQ ID NO. 581:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 59 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

IMPRAPLYRI PLNCNYVLLK SQLVKEELMV SVFVGNTCNT AEFYKGFLLW WAGKKPLKS 59

- (2) INFORMATION ON SEQ ID NO. 582:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 44 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:	
GTLRPRSSDV LPIYLCFTTC LLSLTPNIFT YFSNSACHKF AASP	44
(2) INFORMATION ON SEQ ID NO. 583:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 46 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:	
NVDSCQTHSL ALIPPLLSSS DIVNNDKQLL CTECFFMCCS HFIHMY	46
(2) INFORMATION ON SEQ ID NO. 584:	
(i) SEQUENCE CHARACTERISTIC:	
<ul><li>(A) LENGTH: 41 amino acids</li><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li><li>(D) TOPOLOGY: linear</li></ul>	
<ul><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li></ul>	
<ul><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li><li>(D) TOPOLOGY: linear</li></ul>	
<ul><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li><li>(D) TOPOLOGY: linear</li><li>(ii) MOLECULE TYPE: ORF</li></ul>	
(B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: ORF  (iii) HYPOTHETICAL: yes  (vi) ORIGIN	

(2)	INFORMATION	ON	SEQ	ΙD	NO.	588:
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- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

GKPLVLHATP LSRCPLPLHP TRSLILRPSL HLSDPSFHHY LQRCSYYAPV YRGCPTMTVP 60 SQSNYSSGPK VWLSRAPLPR RGRPFQALPG WNWCRRSLGC IVRPGVGVAS LL 112

- (2) INFORMATION ON SEQ ID NO. 589:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 76 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

GRSREAPAGW PKSTKPPSAR ENPWFSMPHL SPGALCLFTP QEALSYVLLS IYRTPVSITI60 SRDVAIMRPS TGGARR 76

- (2) INFORMATION ON SEQ ID NO. 590:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AGLDQKEELR GVRQHQHQGV RYTRGSSDTS SSPEGLGMAC HAGAMERVKA KPWDPKSNLT60 AKAPSSSGTP CRRAHNSYIS GDSDGNWGPI DGEKDVG 97

- (2) INFORMATION ON SEQ ID NO. 591:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 63 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

NGARLTSQPQ LYQRNHFIQI SQHFQRNTNV YGRVNIRSEN PLEEISVSMF IISAFRGLPV60 WAK

- (2) INFORMATION ON SEQ ID NO. 592:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

(2) INFORMATION ON SEQ ID NO. 593:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 55 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:
AYLFIFLKGK NTFTFSSSPE AQTLLYLTTS QLTPLCDHQC GVVRLKDDSG HMTSL 5
(2) INFORMATION ON SEQ ID NO. 594:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 41 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:
SGDVCTESHC GLSRVKEKEQ QELSLGRWRR GGIDQARPWP W 41
(2) INFORMATION ON SEQ ID NO. 595:

- (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 47 amino acids

  - (B) TYPE: Protein
    (C) STRAND: individual
    (D) TOPOLOGY: linear

  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:	
FKVGLWKGDI VEGERAVLYT YKWYTPFIHG GQRSSDQVTY VQKVTVA	47
(2) INFORMATION ON SEQ ID NO. 596:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 44 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:	
SVLTTSQRLS SHFKSQIPTR AKVLLDLFHP FSTSLSSTLA APSP	44
(2) INFORMATION ON SEQ ID NO. 597:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 1651 base pairs</li> <li>(B) TYPE: Nucleic acid</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: Partial cDNAs produced ESTs by assembling and	
(iii) HYPOTHETICAL: NO	
(iii) ANTI-SENSE: NO	
(vi) ODICIN.	

(A) ORGANISM: HUMAN (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

GAGCTGCCAA GCAGCCCACC TCCTGGGCTT CCCGAAGTGG CCCCAGATGC AACCTCCACT GGCCTCCCTG ATACCCCCGC AGCTCCAGAA ACCAGCACCA ACTACCCAGT GGAGTGCACC 120 GAGGGGTCTG CAGGCCCCCA GTCTCTCCCC TTGCCTATTC TGGAGCCGGT CAAAAACCCC 180 TGCTCTGTCA AAGACCAGAC GCCACTCCAA CTTTCTGTAG AAGATACCAC CTCTCCAAAT 240 GCGCCGTCAT CTACTCCTTG TTCAGCTCAC CTGACCCCCT CCTCCCTGTT CCCTTCCTCC 360 CTGGAATCAT CATCGGAACA GAAATTCTAT AACTTTGTGA TCCTCCACGC CAGGGCAGAC 420 GAACACATCG CCCTGCGGGT TCGGGAGAAG CTGGAGGCCC TTGGCGTGCC CGACGGGGCC 480 ACCTTCTGCG AGGATTTCCA GGTGCCGGGG CGCGGGGAGC TGAGCTGCCT GCAGGACGCC 540 ATAGACCACT CAGCTTCAT CATCCTACTT CTCACCTCCA ACTTCGACTG TCGCCTGAGC 600 CTGCACCAGG TGAACCAAGC CATGATGAGC AACCTCACGC GACAGGGGTC GCCAGACTGT 660 GTCATCCCCT TCCTGCCCCT GGAGAGCTCC CCGGCCCAGC TCAGCTCCGA CACGGCCAGC CTGCTCTCCG GGCTGGTGCG GCTGGACGAA CACTCCCAGA TCTTCGCCAG GAAGGTGGCC 780 AACACCTTCA AGCCCCACAG GCTTCAGGCC CGAAAGGCCA TGTGGAGGAA GGAACAGGAC 840 ACCCGAGCCC TGCGGGAACA GAGCCAACAC CTGGACGGTG AGCGGATGCA GGCGGCGGCA 900 CTGAACGCAG CCTACTCAGC CTACCTCCAG AGCTACTTGT CCTACCAGGC ACAGATGGAG 960 CASCTCCAGG TGGCTTTTGG GAGCCACATG TCATTTGGGA CTGGGGCGCC CTATGGGGTC1020 AGAATGCCCT TTGGGGGCCCA GGGGCCCCTG GGAGCCCCGC CACCCTTTCC CACTTGGCCG1080 GGGTGCCCGC AGCCGCCACC CCTGCACGCA TGGCAGGCTG GCACCCCCC ACCGCCTCC1140 CCACAGCCAG CAGCCTTTCC ACAGTCACTG CCCTTCCCGC AGTCCCCAGC CTTCCCTACG1200 GCCTCACCCG CACCCCCTCA GAGCCCAGGG CTGCAACCCC TCATTATCCA CCACGCACAG1260 ATGGTACAGC TGGGGCTGAA CAACCACATG TGGAACCAGA GAGGGTCCCA GGCGCCCGAG1320 GACAAGACGC AGGAGGCAGA ATGACCGCGT GTCCTTGCCT GACCACCTGG GGAACACCCC1380 TGGACCCAGG CATCGGCCAG GACCCCATAG AGCACCCCGG TCTGCCCTGT GCCCTGTGGA1440 CAGTGGAAGA TGAGGTCATC TGCCACTTC AGGACATTGT CCGGGAGCCC TTCATTTAGG1500 ACAAAACGGG CGCGATGATG CCCTGGCTTT CAGGGTGGTC AGAACTGGAT ACGGTGTTTA1560 CAATTCCAAT CTCTCTATTT CTGGGTGAAG GGTCTTGGTG GTGGGGGTAT TGCTACGGTC1620 TTTTAATTAT AATAAATATT TATTGAATGC T

### (2) INFORMATION ON SEQ ID NO. 598:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3304 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN

**GGAT** 

### (C) ORGAN:

### (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

AAACCCTCTT GGCTGTCTGC TGTCCAGGGA GTCGCCACTC CCTTCATTAT AGCCTTGCTC AGAGTGCAGC GGCAGGCCTG GGGATGGCCT CGGGAGAGGG ACCACAGAGC ACCAGCCTGC 120 ATGGAACTTC CTTCCTCACT CAGCTTCCCA CGTTGCCAGC TGGGACAGGG GAGATGGAGT' 180 · AATTTTGCTG TGGAAAGACT TCACGTCTTG CCGAATGAAA GTCCCGCCTG TCTGTCACGC 240" TGATGCCCGT GCAGCTGTCT GAGCACCCGG AATGGAATGA GTCTATGCAC TCCCTCCGGA 300 TCAGTGTGGG GGGCCTTCCT GTGCTGGCGT CCATGACCAA GGCCGCGGAC CCCCGCTTCC 360 GCCCCGCTG GAAGGTGATC CTGACGTTCT TTGTGGGTGC TGCCATCCTC TGGCTGCTCT 420 GCTCCCACCG CCCGGCCCCC GGCAGGCCCC CCACCCACAA TGCACAAC TGGAGGCTCG 480 GCCAGGCGCC CGCCAACTGG TACAATGACA CCTACCCCCT GTCTCCCCCA CAAAGGACAC 540 CGGCTGGGAT TCGGTATCGA ATCGCAGTTA TCGCAGACCT GGACACAGAG CCAACCGCCC 600 AAGACGAAAA CACCTGGCGC AGCGACCTGA AAAAGGGCTA CCTGACCCTG TCAGACAGTG 660 GGGACAAGGT GGCCGTGGAA TGGGACAAAG ACCATGGGGT CCTGGAGTCC CACCTGGCGG 720 AGAAGGGGAG AGGCATGGAG CTATCCGACC TGATTGTTTT CAATGGGAAA CTCTACTCCG 780 TGGATGACCG GACGGGGTC GTCTACCAGA TCGAAGGCAG CAAAGCCGTG CCCTGGGTGA 840 TTCTGTCCGA CGGCGACGGC ACCGTGGAGA AAGGCTTCAA GGCCGAATGG CTGGCAGTGA 900 AGGACGAGCG TCTGTACGTG GGCGGCCTGG GCAAGGAGTG GACGACCACT ACGGGTGATG 960 TGGTGAACGA GAACCCGGAG TGGGTGAAGG TGGTGGGCTA CAAGGGCAGC GTGGACCACG1020 AGAACTGGGT GTCCAACTAC AACGCCCTGC GGGCTGCTGC CGGCATCCAG CCGCCAGCTA1080 ACCTCATCCA TGAGTCTGCC TGCTGGAGTG ACACGCTGCA GCGCTGGTTC TTCCTGCCGC1140 GCCGCGCCAG CCAGGAGCGC TACAGCGAGA AGGACGACGA GCGCAAGGGC GCCAACCTGC1200 TGCTGAGCGC CTCCCCTGAC TTCGGCGACA TCGCTGTGAG CCACGTCGGG GCGGTGGTCC1260 CCACTCACGG CTTCTCGTCC TTCAAGTTCA TCCCCAACAC CGACGACCAG ATCATTGTGG1320 CCCTCAAATC CGAGGAGGAC AGCGGCAGAG TCGCCTCCTA CATCATGGCC TTCACGCTGG1380 ACGGGCGCTT CCTGTTGCCG GAGACCAAGA TCGGAAGCGT GAAATACGAA GGCATCGAGT1440 TCATTTAACT CAAAACGGAA ACACTGAGCA AGGCCATCAG GACTCAGCTT TTATAAAAAC1500 AAGAGGAGTG CACTTTTGTT TTGTTTTGTT CTTTTTGGAA CTGTGCCTGG GTTGGAGGTC1560 TGGACAGGGA GCCCAGTCCC GGGCCCCATA GTGGTGCGGG CACTGGACCC CCGGGCCCCA1620 CGGAGGCCGC GGTCTGAACT GCTTTCCATG CTGCCATCTG GTGGTGATTT CGGTCACTTC1680 AGGCATTGAC TCAAGGCCTG CCTAACTGGC TGGGTCGTTT CTTCCATCCG ACCTCGTTTC1740 TTTTCTTTCC TATGTTCTTT TGTTCAGTGA ATATCCCTAG AGCTCCTACC ATATGTCAGG1800 CCCTATGCCT CACCCTGAGA ACGCAGTGAG CATGAGGTGG ACCTGTTTGC TGGGAACCCC1860 AGGTCACCCC CTTTTCTTCC CAAACTTGGT GCCTTGGAAG AATCAGGTCC AGCCCTGAAG1920 ATCCTTGGGG AAGAAAATGT TTATGTTGCA GGGTATTGCA TGGTCACGAG TGAGGGGCAG1980 GCCCCTGGGG GACACATCTG CCCACAGCTG CACAGGCCAG GGGCACAGGC ACATCTGTTG2040 GTTCTCAGGC CTCAGATAAA ACCATCTCCG CATCATATGG CCAGTGACCG CTTTCTCCCT2100 TCAAGAAAAT TCTGTGGCTG TGCAGTACTT TGAAGTTTTA ATTATTAACC TGCTTTAATT2160 AAAGCAGTTT CCTTTCTTAT AAAGTGGAAT CACCAAATCT TATCACACAG AGCACAGTCC2220 TGTAGTTACC CAGCCCGCTC CAGCAGTGCG GGAGATTGTA AGGAAGCGGT GGCGGCTGGT2280 GAAGCAAGTC TCACATGTCG GCGTTCTTGG CCAATGGATA CAAAGATAAA GAAAATGTTG2340 CCTTTTCTA GGAACTGTCA GAAATCCTCA TGCCTTTCAA GACTTCTGTG AATGACTTGA2400 ATTTTTTATT CCCTGCCTAG GGTCTGTGAA CGAGGCCTGT CTCTTCCCTG GGGTTTCTTT2460 CCATGGCCTT TATTTCTCCT CTTCCAGTGG GAGTTTTGCA GGCTCTTCTC TGTGGAAACT2520 TCACGAGCGT TGGCTGGGCC TCGGCTTCGC TGGAGTGTAC TCCAGGGTGA AGGCAGAGTG2580 GGATTTGAGA CCCAGGTTAG GCACGACCCA GGCTGAGAAG GGACGTTTCC ATCATTCACA2640 GTGCCTCCC CACAGCAACT ACCTCACCCC GACCCCCACC CTCACTCCTA CCCCACCCG2700 CGATCGTCAG GGGTGCCACG GTGGGCCGGA GGGTGCCGGC TCTGGCTGTC CCTGTGCCGG2760 TCCCTCACAA ACCTCTCCCC CTTTGAAACT CAAGCACAGC TGCGAGGAGG GCAGCGAGGA2820 GGGACCCTC TCTCATGGTT GTCTCTTTCC CCCGCTATGT CATAGGTAGT GGAGGAAGCG2880 AAGGAAGTGA ACGCTGAATG TGACGCATTT CTGAAGAGCT CAGCTGTCAC CGGGCATAGC2940 CTGGAAGCCC CAAGTCTGTT CTGACTTTGC CTGGCTGTCT CCTTGACCCG CCTCCTAGAT3000 CATTGTCCTT GATGTCCAGG CTGGGTCATT TAAAATAGAG ATGCAATCAG GAAGGTTGGG3060 GGACTTGGGA CTGTGGCTGA ATTGAGACCT TGCTGATGTA TTCATGTCAG CACCTGAGTC3120

ACAGCCCAGG TGCCCGGAAG CAGCCTCTTC GCATAGGCAG TGATTTGCGA TTACTTTAAA3180 GCTCACCTTT TTTCTTCCCC TCTCTGTTCG CTGCTGTCAG CATAATGATT GTGTTCCTTC3240 CCTATGGGAT CCATCTGTTT TGTAAACAAT AAAGCGTCTG AGGGAGTGTA AAAAACAGAT3300

- (2) INFORMATION ON SEQ ID NO. 599:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 878 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

GCGGCCGCGC CAGTCTCGCT TCATGACGCA GCCGGTGACC TTCGACGAGA TCCAGGAGGT 60
GGAGGAGGAG GGGGTGTCCC CCATGGAGGA GGAGAAGGCC AAGAAGTCGT TCCTGCAGAG120
CCTGGAGTGC CTGCGCCGCA GCACGCAGAG CCTGTCGCTG CAGCGGGAGC AGCTCAGCAG180
CTGCAAACTG AGGAACAGCC TGGACTCCAG CGACTCCGAC TCGGCCCTGT AAGGGGCGCC240
GCCCGCGGGG GGGACGCGC CGTCCGCGGT CCGCGCGGG ACCGGCGTGT GAACCCCGAG300
AGTGCCCGCG CCCTGCTCCC GGGGGACCCG CAAGGACCCG GGACCGCCG TCCTCGCGCG360
CTCGGACTCC CGCCCGCTG CGAACCGGTC CGTCCTTGTA AATGTTTATT TTTTAACTCT480
TCCCAGTGCG AACTCTGCTG TGAGTGTGT CCGGGGAGGCG CGCCCGCGCT GAGCCGCGCGC
CCGGGTAGCCA CTCCATGCCC TTGTCCGATG GTTTGCAACT CCGATTTTGC ACACCGCTCC600
ACCGTGCCCC CCAGCGCACA CCCATTCACA CTCACGCCAA CACTCTCGCT GAACACTTTT660
ATAATTGTTA GGCGTGGCCG TTGGGACTTT GGGGCGCAGC CGGCTGCTAC TGCGTCTGGA720
GGATTGATAT TTATTTTTGC ATTGCGATGG CTGAAGGCAT TTATTTAACG ATCTTTTTAC780
CTGGATATGT CTGTGAGGCT CCTGAAAGGA AAGAAAAAAA AAAGAAAAAA AAAGAAAAGA AAGAAAAGGT TCGAGAAA

- (2) INFORMATION ON SEQ ID NO. 600:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 2760 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CACCCAACCT	GTGTTGTTGC	CGCCCGGCCC	TTNCCTCCAC	AGNTCTNCTT	NCTNCCGCCC	60
				GGGGCCGGTC		120
				CATCTCTGCC		180
				CCTCGCCTGT		240
				CCTCCAGCAG		300
				CTGGAGGCCC		360
	GGGCCACGTG			CCACCCAGTG		420
				AGCTGTGTCT		
				CTGCGGGCTG		540
			CCATTTCCAT		TACAGCATCC	600
				AACATCCCTC		660
				CCACGGGTGC		720
				GAGGCCGGAG		780
-				AGGGGGTGCC		840
		•		CTGCCCCAGG		900
	ACCTCCCGCG			GTGGCCTCGG		960
				TAGTGTACGA		
				CGGACGTGCT		
•				_		
GTCCCGGCCC				ATGCCTGTGC		
		•		AGGCTGGGCC		
	and the second s		="	TCCTCCCAGA		
	CCGGAAATGT			CAGGCTCTGC		
CTCTGTGAAC				CAAAAAGGGG		
				AGCCGGGGCG		
CCAGGCATGA	CCAAACCTCA	GTGGAGGGC	CTCTGCTTCA	GGCCCCGCCT	GGCTGACATTI	.500
CTGAGCCCCC	CTCGGAGGCC	CCGCCACAGC	CAACCTGCCC	AGTCTTTCCT	CTGGGCTTGA1	560
CCCGCCAGGG	GAGTTCTCCA	GGCCTAGGGC	CAGGAGAGAG	GCCCTGGCAC	CCTGGCGTGG1	620
				TGCTGTCCAT		
CTGCCTGCCA	GGTGAATGGA	CATAGCGTGA	GAGGCGGTGA	GGCCAGGGCT	TCCAGCCTCG1	740
TGCTGTCTCG.	GGACTCCTGA	CCGTGGTGTG	CGTGTGTGCC	CGTCTGTGAC	TTTCTACTCA1	.800
CCAAGGTTGA	AGAAAGGAAA	CGGGGAAAAT	CAAAAGGGGT	TCAAACCCCA	CCTCAGTAGG1	.860
TGGAGGGGAG	CGCCTGCCAT	TGGTTGTATT	TTTGTTCTGA	GTTTTCGGTG	CCGTGTTCCT1	920
AACTACTCCA	TCCCATGACC	TCGCCACACC	TACTGGGGCA	TCTGGCTGGT	GCCTGCTGCC1	.980
ATGGCCAGCC	CCCACTTCTC	ACCCTGCACA	GGGGGTCTTG	CAGCCCCCAG	GCCCACAGCC2	2040
TCGTTGGGAG-	GACAGGGTGG	CCCTGGGGAC	AAGAGGGAGG	AGCCCAGGGG	CTTACCTCAC2	2100
TGAGAGTGCT	CCCCAGCAGG	CATCCACTAC	CCCAGGGCCC	CCCACATGTC	ATGGCAAGGT2	160
TGGTAGTGAA		·		TTGCCCACCC		
CTATGCAATT	CGAGTTCCAA	GCAACATTTG	CTCCTGCCCT	GGGGCCAGCT	CTGCCCCAGC2	2280
				CCCAGACAAG		
GGGGACCAGG	•			TAACCATAAT		
				TAATCTCCTT		
	ACCCCCCGG			CACCCCAGTG		
	GAGGCCTGAA				TGTAGGGCCA2	
•	TACTGTCGCT	,		AACTGGGTTT		
	TTGGGGGCTT					
				AAATCTCGTC		
CIGIGGIII'C	TATTCAGCTT	GGGTTTCATG	ITTAAAATA	AATTTTAAAA	AGCAAAAAAA2	4/60

- (2) INFORMATION ON SEQ ID NO. 601:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1021 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

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GGCGGGGCCG CGAGAGCAGT AGGTGTTAGC AGCTTGGTCG CGACAGGGGC GCTAGGTAGA
GCGCCGGGAC CTGTGACAGG GCTGGTAGCA GCGCAGAGGA AAGGCGGCTT TTAGCCAGGT 120
 ATTTCAGTGT CTGTAGACAA GATGGAATCA TCTCCATTTA ATAGACGGCA ATGGACCTCA 180
 CTATCATTGA GGGTAACAGC CAAAGAACTT TCTCTTGTCA ACAAGAACAA GTCATCGGCT 240
 ATTGTGGAAA TATTCTCCAA GTACCAGAAA GCAGCTGAAG AAACAAACAT GGAGAAGAAG 300
 AGAAGTAACA CCGAAAATCT CTCCCAGCAC TTTAGAAAGG GGACCCTGAC TGTGTTAAAG 360
 AAGAAGTGGG AGAACCCAGG GCTGGGAGCA GAGTCTCACA CAGACTCTCT ACGGAACAGC 420
 AGCACTGAGA TTAGGCACAG AGCAGACCAT CCTCCTGCTG AAGTGACAAG CCACGCTGCT 480
 TCTGGAGCCA AAGCTGACCA AGAAGAACAA ATCCACCCCA GATCTAGACT CAGGTCACCT 540
 CCTGAAGCCC TCGTTCAGGG TCGATATCCC CACATCAAGG ACGGTGAGGA TCTTAAAGAC 600
CACTCAACAG AAAGTAAAAA AATGGAAAAT TGTCTAGGAG AATCCAGGCA TGAAGTAGAA 660
 AAATCAGAAA TCAGTGAAAA CACAGATGCT TCGGGCAAAA TAGAGAAATA TAATGTTCCG 720
 CTGAACAGGC TTAAGATGAT GTTTGAGAAA GGTGAACCAA CTCAAACTAA GATTCTCCGG 780
 GCCCAAAGCC GAAGTGCAAG TGGAAGGAAG ATCTCTGAAA ACAGCTATTC TCTAGATGAC 840
 CTGGAAATAG GCCCAGGTCA GTTGTCATCT TCTACATTTG ACTCGGAGAA AAATGAGAGT 900
 AGACGAAATC TGGAACTTCC ACGCCTCTCA GAAACCTCTA TAAAGGATCG AATGGCCAAG 960
 TACCAGGCAG CTGTGTCCAA ACAAAGCAGC TCACCGACTA TACCAATGAG CTGAAGCCAG1020
```

## (2) INFORMATION ON SEQ ID NO. 602:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2889 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60 GAAAAACTTC CAGATGGCTT CTATCACATC CCCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120 AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGT 180 TCTCTTCATG AAAGTGTTCT TGCCCAAGGA GGAATTGTAC ATGCCCCCAC TGGTGATCAA 240 GGTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTCGTC GGCCAGTGCA CCATCGAGCG 300 CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAAGAG GACATCGTCC CACAGCTCAA 360 AGCCTCCCTG CTGTCTGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA 420 ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGACT GGTGGAGTAA 480 ATTTGATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTCAGA AAGGCTATTC 540 CAAGCTCAAG ATATATAATT GTGAACTAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600 CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660 GGTTGGAGAG TTTAAGGGCT CCTTTCGGAT CTACCCTCTG CCGGATGACC CCAGCGTGCC 7.20 AGCCCCTCCC AGACAGTTTC GGGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780 GATTTACATT GTTCGAGGCT TAGAGCTCCA GCCCCAGGAC AACAATGGCC TGTGTGACCC 840 TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900 CACTCTCAAC CCAGTCTTTG GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAAGAAAA 960 AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA1020 AACAATTATT GATCTGGAAA ACCGATTCCT TTCCCGCTTT GGGTCCCACT GCGGCATACC1080 AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT1140 GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG1200 TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAAATCCT1260 GCACCAGCAC CTCGGGGCCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG1320 GCTGGTCCCT GAGCACGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTTC1380 CCAGGGAAAA CTTCAGATGT GGGTGGATGT TTTCCCCAAG AGTTTGGGGC CACCAGGCCC1440 TCCTTTCAAC ATCACACCCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA1500 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560 CGTCAAAGGC TGGATTCCTG GCAATGAAGA AAACAAACAG AAAACAGATG TCCATTACAG1620 ATCTTTGGAT GGTGAAGGGA ATTTTAACTG GCGATTTGTT TTCCCGTTTG ACTACCTTCC1680 AGCCGAACAA CTCTGTATCG TTGCGAAAAA AGAGCATTTC TGGAGTATTG ACCAAACGGA1740 ATTTCGAATC CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA1800 TGACTACTTG GGTTTCCTAG AACTTGACTT GCGTCACACG ATCATTCCTG CAAAATCACC1860 AGAGAAATGC AGGTTGGACA TGATTCCGGA CCTCAAAGCC ATGAACCCCC TTAAAGCCAA1920 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA1980 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAAATCC TCAACGAGAA2040 GGAGGCCGAC GAGAGGCCAG CCGGGAAGGG GCGGGACGAA CCCAACATGA ACCCCAAGCT2100 GGACTTACCA AATCGACCAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT2160 GAAGTTCATC GTGTGGCGCC GCTTTAAGTG GGTCATCATC GGCTTGCTGT TCCTGCTTAT2220 CCTGCTGCTC TTCGTGGCCG TGCTCCTCTA CTCTTTGCCG AACTATTTGT CAATGAAGAT2280 TGTAAAGCCA AATGTGTAAC AAAGGCAAAG GCTTCATTTC AAGAGTCATC CAGCAATGAG2340 AGAATCCTGC CTCTGTAGAC CAACATCCAG TGTGATTTTG TGTCTGAGAC CACACCCCAG2400 TAGCAGGTTA CGCCATGTCA CCGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCCTGGAAA2460 GTCAGGCCAA CAAGCAACGT TTGCATCATG TTATCTCTTA AGTATTAAAA GTTTTATTTT2520 CTAAAGTTTA AATCATGTTT TTCAAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580 CATCTTTTTA TATGTGTCTT CGGTTCTAGA CTTCAGCTTT TGGAAATTGC TAAATAGAAT2640 TCAAAAATCT CTGCATCCTG AGGTGATATA CTTCATATTT GTAATCAACT GAAAGAGCTG2700 TGCATTATAA AATCAGTTAG AATAGTTAGA ACAATTCTTA TTTATGCCCA CAACCATTGC2760 TATATTTTGT ATGGATGTCA TAAAAGTCTA TTTAACCTCT GTAATGAAAC TAAATAAAAA2820 TGTTTCACCT TTAAAACATA GGGGGGGTGG TCGGGGGGGTC GGGAGGGGGG GGGGTGGTC1880 GGGGTGTGG



- (2) INFORMATION ON SEQ ID NO. 603:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 3638 base pairs
    - (B) TYPE: Nucleic acid (C) STRAND: individual

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG 60 GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG 120 GCTAAAACAT TGCACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA 180 ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACGAAGAGT 240 CCCATATTTG GTCCCGAGGA GGTGAATAGT GTGGAAGGTA ACTCAGTGTC CATCACGTGC 300 TACTACCCAC CCACCTCTGT CAACCGGCAC ACCCGGAAGT ACTGGTGCCG GCAGGGAGCT 360 AGAGGTGGCT GCATAACCCT CATCTCCTCG GAGGGCTACG TCTCCAGCAA ATATGCAGGC 420 AGGGCTAACC TCACCAACTT CCCGGAGAAC GGCACATTTG TGGTGAACAT TGCCCAGCTG 480 AGCCAGGATG ACTCCGGGCG CTACAAGTGT GGCCTGGGCA TCAATAGCCG AGGCCTGTCC 540 TTTGATGTCA GCCTGGAGGT CAGCCAGGGT CCTGGGCTCC TAAATGACAC TAAAGTCTAC 600 ACAGTGGACC TGGGCAGAAC GGTGACCATC AACTGCCCTT TCAAGACTGA GAATGCTCAA 660 AAGAGGAAGT CCTTGTACAA GCAGATAGGC CTGTACCCTG TGCTGGTCAT CGACTCCAGT 720 GGTTATGTGA ATCCCAACTA TACAGGAAGA ATACGCCTTG ATATTCAGGG TACTGGCCAA 780 CGACTGTTCA GCGTTGTCAT CAACCAACTC AGGCTCAGCG ATGCTGGGCA GTATCTCTGC 840 CAGGCTGGGG ATGATTCCAA TAGTAATAAG AAGAATGCTG ACCTCCAAGT GCTAAAGCCC 900 GAGCCCGAGC TGGTTTATGA AGACCTGAGG GGCTCAGTGA CCTTCCACTG TGCCCTGGGC 960 CCTGAGGTGG CAAACGTGGC CAAATTTCTG TGCCGACAGA GCAGTGGGGA AAACTGTGAC1020 GTGGTCGTCA ACACCCTGGG GAAGAGGGCC CCAGCCTTTG AGGGCAGGAT CCTGCTCAAC1080 CCCCAGGACA AGGATGGCTC ATTCAGTGTG GTGATCACAG GCCTGAGGAA GGAGGATGCA1140 GGGCGCTACC TGTGTGGAGC CCATTCGGAT GGTCAGCTGC AGGAAGGCTC GCCTATCCAG1200 GCCTGGCAAC TCTTCGTCAA TGAGGAGTCC ACGATTCCCC GCAGCCCCAC TGTGGTGAAG1260 GGGGTGGCAG GAGGCTCTGT GGCCGTGCTC TGCCCCTACA ACCGTAAGGA AAGCAAAAGC1320 ATCAAGTACT GGTGTCTCTG GGAAGGGGCC CAGAATGGCC GCTGCCCCCT GCTGGTGGAC1380 AGCGAGGGGT GGGTTAAGGC CCAGTACGAG GGCCGCCTCT CCCTGCTGGA GGAGCCAGGC1440 AACGGCACCT TCACTGTCAT CCTCAACCAG CTCACCAGCC GGGACGCCGG CTTCTACTGG1500 TGTCTGACCA ACGGCGATAC TCTCTGGAGG ACCACCGTGG AGATCAAGAT TATCGAAGGA1560 GAACCAAACC TCAAGGTACC AGGGAATGTC ACGGCTGTGC TGGGAGAGAC TCTCAAGGTC1620 CCCTGTCACT TTCCATGCAA ATTCTCCTCG TACGAGAAAT ACTGGTGCAA GTGGAATAAC1680 ACGGGCTGCC AGGCCCTGCC CAGCCAAGAC GAAGGCCCCA GCAAGGCCTT CGTGAACTGT1740 GACGAGAACA GCCGGCTTGT CTCCCTGACC CTGAACCTGG TGACCAGGGC TGATGAGGGC1800 TGGTACTGGT GTGGAGTGAA GCAGGGCCAC TTCTATGGAG AGACTGCAGC CGTCTATGTG1860 GCAGTTGAAG AGAGGAAGGC AGCGGGGTCC CGCGATGTCA GCCTAGCGAA GGCAGACGCT1920 GCTCCTGATG AGAAGGTGCT AGACTCTGGT TTTCGGGAGA TTGAGAACAA AGCCATTCAG1980 GATCCCAGGC TTTTTGCAGA GGAAAAGGCG GTGGCAGATA CAAGAGATCA AGCCGATGGG2040 AGCAGAGCAT CTGTGGATTC CGGCAGCTCT GAGGAACAAG GTGGAAGCTC CAGAGCGCTG2100 GTCTCCACCC TGGTGCCCCT GGGCCTGGTG CTGGCAGTGG GAGCCGTGGC TGTGGGGGTG2160 GCCAGAGCCC GGCACAGGAA GAACGTCGAC CGAGTTTCAA TCAGAAGCTA CAGGACAGAC2220 ATTAGCATGT CAGACTTCGA GAACTCCAGG GAATTTGGAG CCAATGACAA CATGGGAGCC2280 TCTTCGATCA CTCAGGAGAC ATCCCTCGGA GGAAAAGAAG AGTTTGTTGC CACCACTGAG2340 AGCACCACAG AGACCAAAGA ACCCAAGAAG GCAAAAAGGT CATCCAAGGA GGAAGCCGAG2400 ATGGCCTACA AAGACTTCCT GCTCCAGTCC AGCACCGTGG CCGCCGAGGC CCAGGACGGC2460 CCCCAGGAAG CCTAGACGGT GTCGCCGCCT GCTCCCTGCA CCCATGACAA TCACCTTCAG2520 AATCATGTCG ATCCTGGGGC CCTCAGCTCC TGGGGACCCC ACTCCCTGCT CTAACACCTG2580 CCTAGGTTTT TCCTACTGTC CTCAGAGGCG TGCTGGTCCC CTCCTCAGTG ACATCAAAGC2640 CTGGCCTAAT TGTTCCTATT GGGGATGAGG GTGGCATGAG GAGGTCCCAC TTGCAACTTC2700 TTTCTGTTGA GAGAACCTCA GGTACGGAGA AGAATAGAGG TCCTCATGGG TCCCTTGAAG2760 GAAGAGGGAC CAGGGTGGGA GAGCTGATTG CAGAAAGGAG AGACGTGCAG CGCCCCTCTG2820 CACCCTTATC ATGGGATGTC AACAGAATTT TTTCCCTCCA CTCCATCCCT CCCTCCCGTC2880 CTTCCCCTCT TCTTCTTTCC TTACCATCAA AAGATGTATT TGAATTCATA CTAGAATTCA2940 GGTGCTTTGC TAGATGCTGT GACAGGTATG CCACCAACAC TGCTCACAGC CTTTCTGAGG3000 ACACCAGTGA AAGAAGCCAC AGCTCTTCTT GGCGTATTTA TACTCACTGA GTCTTAACTT3060 TTCACCAGGG GTGCTCACCT CTGCCCCTAT TGGGAGAGGT CATAAAATGT CTCGAGTCCT3120 AAGGCCTTAG GGGTCATGTA TGATGAGCAT ACACACAGGC ATGAGCCACT GAGCCTGGCC3180 CAGAAGCGTT TTTCTCAAAG GCCCTCAGTG AGATAAATTA GATTTGGCAT CTCCTGTCCT3240 GGGCCAGGGA TCTCTCTACA AGAGCCCCTG CCCCTCTGTT GGAGGCACAG TTTTAGAATA3300 TCTGTCACTC ACATGGACCC AAGATAAAAG AATGGCCAAA CCCTCACAAC CCCTGATGTT3420 TGAAGAGTTC CAAGTTGAAG GGAAACAAAG AAGTGTTTGA TGGTGCCAGA GAGGGGCTGC3480

TCTCCAGAAA GCTAAAATTT AATTTCTTTT TTCCTCTGAG TTCTGTACTT CAACCAGCCT3540 ACAAGCTGGC ACTTGCTAAC AAATCAGAAA TATGACAATT AATGATTAAA GACTGTGATT3600

GCCACCAAAA AAAAAAAAAA AGACGAAAAG AAAAAGGG

- (2) INFORMATION ON SEQ ID NO. 604:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 2775 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual
    - ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

ATAGGTTTGG ACCTTTCTTG GTAGAATTAC TGCCCTAATT TTGTTCCACT GATACTAGAA 60
ACGGTCTGAT GTTAGAGCTG GAAGGGATCT GTAGTATCAC GCAGTCCGAT TCTCTAATTT 120
TCCACATGAG AAAATGAAGG TCCAGAGGAA GCAGAGACTT AACTCACAAA TCAGAAAAGC 180
GGTTCTTGCA GAACTGAGGC CATAGTGAGG ACTTTCTGCT TTCCACCATA CCACCTTGCC 240
AGTCCACACA AGAGGGAGGA TGTATTTTGG GGGGCATACA CTGAGGATGG AGAAAGATGG 300
CATCAGAACT GCTGGGTGAA GTGGTGCTT AACTGGACTT TGACAGCTGC CTTTTGAAAA 360
CCCCAAAACT AAACACACTG CATGTAATCA AAAGATGCTT ATACTAATAA TGACCTGTGC 420
TGTTCCCACT CAGTTGCTCT CTGTTTTCGA GAAGACATGA GAAGCTGCAA CATGACCTGG 480
AGTGGAACTG GAGGTCACA TTTTTTTTT AGCCACTTGC TGGCCAGCAC AGCGACTGCA 540
CCCTCCCAGA AGGCTGAAGT GCTCGTGTGC TGCACCTCCA TGGCATCTCT GCAGTGGTCA 600
GAGTGACCTG GTATAAGGGA GAGGGCATCA CCTTGCCCCC TGTGCTGACT CCTGCCCTTC 660
CCCTACAGGA GAGTCCATCC CGATCCGGCT CTTCCTGGCC GGGTATGAGC TCACGCCCAC 720
CATGCGGGAC ATCAACAAGA AGTTCTCTGT GCGCTATTAC CTCAACCTGG TGCTGACAT 840
CGTACGGAAG AGCATGTCCC ACCAGGCGC CATCGCCCTCA CAGCGCCAC 720
CATGCGGGAC ATCAACAAGA AGTTCTCTGT GCGCTTATAC CTCAACCTGG TGCTGACAT 840
CGTACGGAAG AGCATGTCCC ACCAGGCGC CATCGCCTCA CAGCGCTTTT AGGGCACCAC 900

CTCCCTGGGT GAGGTGCGGA CCCCCAGCCA GCTGTCTGAC AACAACTGCA GGCAGTAGGC 960 CCCCAGGGCC GAGAAGATGC TGGGCACCCA CCCAGCACCC CCATCTACCA ACACCAGCGG1020 CTGGGGGCGG GGGCGGACCT TGTGAGGCTC AGTTGACCCG TTACTTGCAA CCTGAAAACA1080 AATCATGTTT TTGACTTAAA TTCTTTTCTC TGGAGAACCC AAGGGGCTTG GGGTGGGAAG1140 CAGTCTCTCC TTGGGATTCT GCGGCCGATG TGGGATAGAA GAGGTAGCAT CCTGGAAGCC1200 AGCCTCTCTG GGGAACATGA GCCCCCTTCC TCGGGGGGCT GCCTTGCGTC TTAGAGGAGG1260 GAGAGCAGAG AGCACGCATC CTTGGCTCCT GGCTCTCTGA GCTTCCTGAT ACAGGATCTG1320 AGCATGTCCC TGGGATTCTG AGCTGCCAAC AGGGCCCTGG GTAGTCACAT CTTGTACTCC1380 CCTTTGCTGT CCCGGAGGTA GTGGCAGGAG TTGGGCCAGC CCCCACTAAG TGGCAGGGGA1440 AGACTCACGA TTGGGAAGCT ACCTCTTTGG GAATCTTGGA TGTGGTGATC TCAAGTTCCC1500 ACAGGCCACC TCCTTCTGGC CACTCACTGC TGGGACCCAG GCACCTCCCT TCTCCATCCT1560 CTCTGGATTG TCAGTAATGT CCTGGAACAG AAGCCTGTAG GATGGCCTTG GGCACGGAGA1620 AGCCCTGGGG TCAGTGTCGT GCACGGATGG CGGCAGTGTT GAACCCAGGA GGCTGAACCC1680 GGCCCACCAC GGAAGATGAG TGCATGGCAA CCGCCTGCCT TCACGTCGCT CCACTTGGTA1740 ACCCCAAGGT CTGGGCTGTT CTAGGTATTG CTTCACGTGC CCCAGCAAGC CCTTAACAAG1800 AGGGCCTGGT TCCCTGAAGA ACCAATCCCA GGAAGGGGCC TTGATCCCTC CGCCTTGCTG1860 CGAACCTTTG GCAAGGCTGT TCTTACTAAT GCCCAAGCCC CTTTACCCCT CTCCCTATAG1980 GTTACACAGG GGAGACCAGG GCCTCGGCAG AAGACTGCTG CCACACTTCC GAATCATTCT2040 GCTTGCCAAA TAGGTCATCT TCACCAGTTG ACTGACCCAA GTTTAGGACC ATTGGTATCG2100 TGTGTTTAAA AAACACATAT AAAAAAACTC TTGTGAATAT TCTTGTTATG CTAGAGAGGA2160 AGGTACTTCT CCCTCTACGG CTCTGCGCTG GGGCCTATGG TAGTAAAGTT GTTTACTGTC2220 CTTTTTCTGC TTCCCCTGGA AATGACAGGC ATTACTCTCC CATTGGCCTC CCTTCCCTTT2280 ATAGAAAGAC CAAGCAGGCC CCACTGGCCA AGAGGTACGG TATTTGGCAG TCTGAGTTCT2340 CAGTAATTTG GAAAGTTAAG GAGTTGGTTC CTGTGTCACC TTTCAGTTAG TGTGGGAAAG2400 GAAGACTTCT GTTTTCCTGA GATCAGTGCA GTCTCAGGCC TTTGGCAGGG CTCATGGATC2460 AGAGCTGAGA CTGGAGGGAG AGGCATTTCG GGTAGCCTAG GAGGGCGACT GGCGGCAGCA2520 GAACCGAGGA AGGCAAGGTT GTTTCCCCCA CGCTGTGTCC TGTGTTCAGG TGCGACACAC2580 AATCCTCATG GGAACAGGAT CACCCATGCG CTGCCCTTGA TGATCAAGGT TGGGGCTTAA2640 GTGGATAAGG GAGGCAAGTT CTGGGTTCCT TGCCTTTTCA GAGCATGAGG TCAGGCTCTG2700 TATCCCTCCT TTTCCTAGCT GATATTCTAA CTAGAAGCAT TTGTCAAGTT CCCTGTGTGG2760 CCCTTCCCCC CAGAG

- (2) INFORMATION ON SEQ ID NO. 605:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 944 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:

- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

- (2) INFORMATION ON SEQ ID NO. 606:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1939 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

CCAGTCAAGA	ATCTCCCACT	AAGCTTCAAA	GTAGTGGATT	ACAGCATGGC	AACCATGCCA	60
GTAATTTGAA	ATTTAGTAGA	GAGGCTTTCG	CTTAGTAGAG	ATGGGTTTTT	GCAGGCTGCT	120
CCCGAACTCC	TGACCTCACC	CCACCGGGG	CAACCCCCC	ATCGGGCCCC	CAAAGTGCTG	180
GGGTTACAGG	CTTAAGCCAC	CAAGCCCGGC	CGACCTTCTT	CTATTTTTCC	ATTCTCCTTT	240
CCAAAGCCAT	GGCCATGCGC	TCCTGTGTAC	AGGTGCATAA	ACACATCAGT	GTGCCATCCC	300
TCACATGCAT	GTCGTTCCCC	ACCCCTCCTT	CCCAGGGCTT	CTCTTGGCTC	CAGCGTTCCT	360
CTGGGACCCT	CTGCAGATAC	AGCCTGTGCT	GGACCCCCAG	CCAGGGTGAG	GGCTCATTCT	420
GCTCTGTCTT	CCCCACTGCC	TCAGTTTCCC	CCAAAAGCTG	ETTTCACGTC	CTTCTAGTAG	480
GGGGCCTCCC	ATGGGGGCAA	GGATCCCCTT	TAGGATTCAA	TCTTTCCTCT	TTGGGCAGTT	540
TTGGCTTTGA	GTCCCCCAGG	GATCAGGGTG	AGAATGAAGA	AGAGCTCAGT	GAGCGGAATG	600
ACAGCAGCTG	GGTGGGTGGT	GTGGGGAGAG	GCTGAGGGGA	AGGCAGCTCT	AAGACTGGGA	660
GTGGAGTTCC	TGGAGGTGTG	GGGAGGGGG	CGTGTTTTCA	ATTTAGAAAA	ATCTCAGCCA	720
GCTCGAGCCG	AGAGAGAATG	CGAAAGAGGA	AGTTCGGAAG	GAGCGAGGAA	TGGGGTGGGT	780
GGCAGCGGGG	GCCGCTCAGT	CGCTGTCGCT	CTTGTCCACC	AGCACGGCGT	CCGACTCCTC	840
GGTGATCTCC	AGCAGCGCGT	GCACGTCGGG	GCTGCTCCCG	CGCCGCAGGT	CGCCGGCCTC	900
CCCCCGCTCC	GCGCCGCCCT	CGTCGTCGTC	GGCGCCCACC	TCCACCATCT	CGGTGGCCTT	960
GAGCACTTCC	ACCTGGCCCT	CGCGGATCTT	CTTGACGTGG	AAGGTGAAGG	GTGGCACCTT:	1020
GTAGACCGCG	GTCTTGGAGC	GCGCGTACAC	CACGTGGTCG	GGCGTGAAGG	ATTTGCGCAA	1080
CTTGTCCCGC	GACGTCTTCA	GTTTCTCGCG	CCGCTCGGCG	GGCACCAGGC	GCGTGCCCAG	140
CTTGTTCATG	CGCTTCTCCA	GGGTGTGCCG	CGTCTTCTCC	AGGTTTTCCT	TGGTCTTGAG	200
GCGCGTCTTC	TCCAGGTTCT	CGCGGGTACG	CACCTTGGTC	TTCTCCATCT	TCTCCTTGGAI	260
GAAGGCCTTC	TTGAAGTCGT	CCACGCGCCG	CAGGCCCTGC	GCTTGATACG	CTCTGCGCGG1	320
GACTCCTCAA	TAACCTCCTC	AACCTCCACC	GCCTCGTCCG	ACGAAAGCTC	CAGCGCCGCTI	1380
GCGTCCTCCT	CGGGCCGCTC	GCCCTCGCCC	AGCTCCTCGC	CCTCCTTCTC	TGGCAGCGCC1	440
TCCGACTCTT	TCAGCGATTT	GCTGATGCTC	AGTTTGGCCG	GCAGCTTCAC	TTCATCCTGG 1	5.00
TAGATCATGA	CTTTAAAGTT	GCGGCGCCGC	AGCAGCTCGG	CCTCGTTGAC	CTCCAGCTTC1	5.60
TTGATCTGCC	CCGCCTGGCG	CTCCAGGCTG	CCGCGCACGG	TCTTCACGTT	GACGCTGACC1	.620
TTGCGCACCT	TCTCCAGCAG	CTTGCTCACC	GTATTGCTCG	TGGTGGCGTG	CGCCTTGCCC1	680
AGCTTGCTCA	GCTCGCCCTG	GATGCTCTGC	ACTGCGCCCT	CCATCTCCGC	CTGCCGCTCC1	740
TCCAGCTGTG	CTTGAGTCAG	CTGGATCTGG	TCTACGGCCC	CGATGATTTT	GTCCAGGAGG1	0.08
CTCAGCACCA	GCACGCCGTT	CACCTGGTCC	GACTTGATCA	GCTCTTCTGA	GCCGGCCCCC1	860
GACGGCTCCT	CCGCTGCCTG	AGCCCCAGCG	GAGGAAGCTC	CGGGGCCTCG	GCGATCGGGG1	.920
TACCCGGGCA	AGCGGCCGC			•	1	.939
	and the second s					

- (2) INFORMATION ON SEQ ID NO. 607:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1570 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

GGCACGAGGA AGTTAAGATC ATACATGCGG ATGTGCTGGT AACCTGCAAG AAGCAATCAT

GCTGCGGTCC	GGTGTGACCT	CCCAAGGCAT	TCACCCTGGG	AGTCCCTGGT	GCTGCACCCC	120
AACCCAGGCA,	GAGCTCATCG	TGGGTGACCA	GAGCGGGGCT	ATCCACATCT	GGGACTTGAA	180
AACAGACCAC	AACGAGCAGC	TGATCCCTGA	GCCCGAGGTC	TCCATCACGT	CCGCCCACAT	240
CGATCCCGAC	GCCAGCTACA	TGGCAGCTGT	CAATAGCACC	GGAAACTGCT	ATGTCTGGAA	300
TCTGACGGGG	GGCATTGGTG	ACGAGGTGAC	CCAGCTCATC	CCCAAGACTA	AGATCCCTGC	360
CCACACGCGC	CGTACGCCCT	GCAGTGTCGC	TTCAGCCCCG	ACTCCACGCT	CCTCGCCACC	420
TGCTCGGCCT	GATTAAGACG	GTGCAAGATC	TGGAAGGACG	TCCAACTTTC	TCCCTGATGA	480
CGGAGCTGAA	GCATCAAGAG	CGGCAACCCC	GGGGAAGTCC	TCCCGCGGCT	TGGATGTGGG	540
GGCCTGCGCT	CTCATCGGGG	GACTCCCAGT	ACATCGTCAC,	TGCTTCCTCG	GACAACCTGG	600
CCCGGCTCTG	GTGTGTGGAG	ACTGGAGAGA	TCAAGAGAGA	GTACGGCGGC	CACCAGAAGG	660
CTGTTGTCTG	CCTGGCCTTC	AATGACAGTG	TGCTGGGCTA	GCCTGTGACC	CCTCGGGACN	720
TGCCTGGTGC	AGGTGGTGGC	AGCNTGGAGG	GACCCATGCA	GCACCCAGGT	CAGAGCAGAC	780
CCNTNCCCCT	NGCCNGGCCT	GCGCCANGCT	GGNACCTGAT	GGCCCCCTGT	GGCGCCTTGA	840
CCTGCTGGGC	CAGGCTGNCC	CTGGGACTCT	CAGCCCCCAN	GTTGCTTATC	CANGATGTGA	900
CAGAGCTCGA	CCCAAGCCAG	GCTGCACACT	CCTGGACNTG	GGCTAGCCTG	CACTGCCNTG	960
GGAAAGNTCN	GCCGAGGGCC	CANAAGCTGC	TGAGGGGTNC	TGAGGCTGGT	GCCCACCCCC	.020
AAGCTAGTGT	GTTCTCTGCC	CCTCCCTGCC	CGCGTTTCAG	GGCCTCGGTC	CATAGAGAAC	080
				CCAGCAGCTG		
				AGGCTGGGCC		
CTCAGTCTGG	GAGGTAATAA	AAGCAGACCG	ACACGCAGAT	GTTGCTCGGG	AAAAAAAAA	1260
AAAAAAAAA	AAAAAAAAGC	CGCTGTCTCC	GGGGCCCCTC	TGCTCGCCGG	GCCCAGTAGA	1320
TGGGGGTCCT	CATGCACAGG	CGCTGCACCA	. AAGCCCCCGC	CTGGGCGGTA	GCCACTTACG	1380
AGGCTCCCCT	GCACTGCCAG	CAGCTCCTGG	GTGTGGTGGG	TGTCCTGGCT	GGGGACCCAA	1440
				CTCCCGATCA		
TCAGGCGGAG	GAAGCAGACC	TGGTGCTCCT	CAGGGCGGTA	ACAGATGCAG	CCGCTCTGCC	1560
CGTCGAACAG				•		1570



- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1768 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) ANTI-SENSE: NO

(iii) HYPOTHETICAL: NO

- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

GCACAATCCC GGCTCACTGC AACCTCCAAC TCCTGGGTTC AAGCGATTCT CCCGTCTCTA 60 CAAAGTATAC AAAAAAATTA GCCAGGCATG GTGGTGCGTG CCTGTAATCC CAGCTACTTG 120 GGAGGCTGGG GCACAGGAAT CCTTTGAACT TGGGAGGCAG AGGTTGCAGT GAGCTGAAAT 180 CACACTACTG CCCCCCAGCC TGGGCAACAG AGCAAGACTC TGTCTCGAAA AAAAAAAAA 240 AAAACAATGA AGGAAAAGGA GGGTGAGTTA GCTGGAGTAG AATAGAGGTA TAGAATCGTT 300 CCTAAATAAC CGGCTGCATT GGTTTCCTGG AGACTTGCTA AAAACCCAGA TTCCCAGGCC 360 CCACTTCTTG GTGCTCCTAA TTCAGTAGCA TCACAGTAGG GTTCCAGAAG CGGTATTTTT 420 AACAAGCTCC CAGGTAATTC TGATGTGCAC CTAGATTTGG AAATCACTGT GTTAAAAAAT 480 ATTGTGAGGT AAGTTGGTCA GTTAGGTTGG GCAGCTTTTA TTTCATTGCT AAGGGATTTG 540 GACTTGATGG TGTAATAAAG CATTAATTGA ACAAATATTT ATGGAGCCTG TACTATGTAC 600 CAGATGCAGA CTGTGCTAGC GGTTGGGGAT ACAGTGATGA CTTGGTCTGC CTCTAGGTGG 660 CAGGGAGCCA TTTTGGGTTT TCGAACAGAA AAGTGACATA ATGAATGCTG AGTTCTTAGG 720 AAGATTAATC CAGGAGTAGT CTCCAGGATG TACTGGAAGG AGAGAAGCTG AAACCAGGGA 780 GGCTGCTGTG TTTGCAGTTG GCTGCCCAGT GCTACCTCTG CAGAGACAAT CAATGTCCTG 840 AAGGTAGCTG GTATGTCTGT GTGCACTGAC ACGAGCCTTC CTACCAAGCC CCAGGGGCTC 900 CATGCTGGAG AATGCACGTA GGGCTAGGGT GAGCACTAAC TTCACTTCAG GAGAGCAAGG 960 AACAGTGTGG CTCTTCCATT TTTCAGTTCT GTAAGCACAT CACCCTTTTC TCCTCCCCTT1020 GAGCTGTGTT CTCTGACAGC TGTTTGTTGG TAAAGCCAGC AGCCCCTAAA GCACGTCCCA1080 GCCTTGTCTC CTCTGTGCTT TCCCCCACCA CTGCTGCTGC ACGCCTCATT TGCTGGGCCA1140 CTTTAGTGGT GGAACCATTA GAGGCTGAGT GACTTAAAGG AGATTGAGTC TGTCTCGACC1200 CCGAGAGAGA GTGGGATGGA TGGATGCATC GTCTCATTTA GAAAGTGTTG CCTCTGACTC1260 TAACACACTC TTCTCTCTTT CTTTACCGCC CTCCCTGTGT GCGTCCCTGG GGGGGCGTGG1320 GCTAAACCCC TTCCGTCCCC CTTTCTCCTT CTCTCTCACA GTGTAGGCAC CACTTCTCTT1380 ACAATTTAGG CTTTCTCTCT GCCTTGGGCT GAGTGAGGAA GAGGAGTGCT GTTCCTGCCT1440 TCCTAGCCCA GCTGGGTCTG ACCAGAGGCT ACTGTGTACC CATTTACCAT GCGTGATTGT1500 TAACTCAGAG TGGGGTGTAG CCAGGTATTG ACTGAATGTA TGTTCTTGCT GACCTGTGTT1560 TTTTTCTGTA GGGACCAAAG CAGTATCCTT ACAATAATCT GTACCTGGAA CGAGGCGGTG1620 ATCCCTCCAA AGAACCAGAG CGGGTGGTTC ACTATGAGAT CTGAGGAGGC TTCGTGGGCT1680 TTTGGGTCCT CTAACTAGGA CTCCCTCATT CCTAGAAATT TAACCTTAAT GAAATCCCTA1740 ATAAAACTCA GTGCTGTGTT AAAAAAAA 1768

- (2) INFORMATION ON SEQ ID NO. 609:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1001 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

TAAGGAGACT GAAAGGTGAT TCATTTAGTG AGTAGCGATT ACAGAATTTC TAAAACAGTG GGGGCGGGG GGGCGGGG GAGGAGGCT GGAATTGTCC TCCAGCGCAT ACAAGGTTGT 120 TGCTGCCAGA GAAATCCAGC AGGAAAGAGC AGCATTCTTT CACCTTTTCC GCCTCTGAAG 180 CGGAGGAGAA CTTCATTTCC CAGCAGCCCT TAAGATTCCT CCGCGCACTG CGTAGCGTCT 240 CCGGCATTCT GCTTTCCGGC GCTCTGCCTT CCGGTGCGTC GTTTACGGCC AGTTTGAACC 300 AAAGACGCCC AANGGTTGAG GCCGAGNTTC CAGAGCATGG GGTCTCGGTT GTCCCAGCCT 360 TTTGAGTCCT ATATCACTGC GCCTCCCGGT ACCGCCGCCG CGCCCCCAA ACCTGCGNCC 420 CCCAGCTACA CCCGGAGCGC CGACCTNCCC CNAGCAGAAC ACCGCCTNGT TGAAGANCCT 480 GCTGGAGCTG TCGNCGTNGC TTTCTGGGTT GGGGCTGATG GGGGNNCGGG CGGGTACGTG 540 TACNTGGGTG GCANCGGAAG CCCATGAAGA TNGGGATACC CCCCGAGTNC CATGGACCNA 600 TTACNGCAGA TGGTCATCGN NGCCTCANGC NATTGCCACC TNGGGGTANT CGTTGTNCAT 660 NGGCAGACCC CAAAGGGAAN GGCCTANCCG CGTTGTTTNG AAAGNTACCA CCANGTGAAT 720 NCTGTCTTCT GTCTNCTNGT CCCNTTTNCC CCGTGACACA CAGAGCAGGC ATGGAATTTA 780 ATGGGNTGTT CTGGNACNAG ACACTTGTAC ATGGACAGAC ATCACTACTN NGTGGATACT 840 NNACAAGACT GAAAAGNAAA ATCGTATGTT GTCATTCNTC TGGCTANTGG AGTGTTTGTG 900 GCCTTCACAG ATTTCACAGG AACCAATAAA TCCCTCAGAG AAGTAAAAAA NAAAAAAAAA 960 А АААААААА АААААААА АААААААА АААААААА

### (2) INFORMATION ON SEQ ID NO. 610:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2515 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

GGTGTGGAAA CTACTGCAAA TAGTAGCACT TCACTGAGAT CTACAACTCT TGAAAAAGAA 60 GTTCCTGTCA TCTTCATCCA CCCTTTAAAC ACTGGATTAT TCCGGATAAA AATTCAAGGA 120 GCCACTGGAA AATTTAATAT GGTCATCCCT CTTGTGGATG GGATGATTGT CAGCAGGCGA 180 GCTCTTGGCT TTCTGGTGAG GCAGACTGTA ATTAACATTT GTAGAAGAAA GAGACTGGAA 240 AGTGACTCCT ACAGTCCCCC CATGTCCGCC GGAAACAGAA AATCACCGAC ATTGTCAACA 300 AGTACCGGAA CAAGCAGCTG GAGCCAGAGT TTTATACTTC ACTTTTCCAG GAGGTTGGAC 360 TCAAGAACTG CAGTTCTTAG ACCACTGAAT TTCTAAGACT GTTGAACTCC AGTTTGGGAA 420 CTATAACACA GCAGAACAGT TTGATAGGTG ATCACTGTAA AAATAAAAAC AAATCACTCC 480 CAAGAGCTTA CTGTTTAATC ACCAGAATAG AAGAAACACA TTATAACCCA TTTGATAGAA 540 GACTTTGGGC TATCTAGTGA AATGGGCTCC CAGACACAAT CATACTCCTG CTGATAATGA 600 TGATATACAT TTTAGCCATA AACTTTCTTT TAAAAGTGAC AATTTTAGTT AAACATAAGC 660 CTTTTGAGGA GAAAGGCTTT TATGCATCTC AGTTAAACAC GTGCATTGGT AGTATCAACA 720 AATTTGCAAT ATAGAAGTTG AAGATAGTTT TTTNCCTCAC TTTTTAGGAG GCTGTATTCA 780 AAATTAAAAT CTCAGAATCT TACAGGACAT TTAAAGGACT CATGTTGATA GCATGGAGGA 840 GAAGGAAAGA AGTCACAGCC TTCTACTCAG TTGTAGGTCT TCTTGTCATC CAGCTGTCAC 900 ACTGACAAAA AGAAAAGATG ATANCATGTT TTTTTGCTCA GATAAGAAGC CTGACATTAA 960 AAGATGTCAT ATTTTTTCT CCACATTTCA AAAAGTTGTC CTTCTCATCA CTGCACAGAT1020 CTGTCTGAAA GCCTCAGTTT CTGAGTGACC CAGGAACAGA TCAGAAATGG AGCATGGCCT1080 TGTCCTTTAA TGGGGATGCA AATAAAGTTT GTGGGGTTAA AAGTTATAAG ACAGCAGTGA1140 TACCCCACTC TCTCCATTAT TGTCCAGCGG GGTGACATAA TGACAGGTTA AATATTTGTG1200 ATTCATTGAT TAAATATTAT TTAAAGAAAT GTAAAAAAA AAAAAAGGTT GAAAATTATT1260 TGGTTTCATC CATTGTCTCT TATTTCAGGA CCAAGCAGCA AACTGCAGTA GTTTGTGAAG1320 GATTCTAATA TGGGGTTCAG GAATAGCCTC TCAACGCTAC TAATTCAGAT CTCTCCCAGA1380 GAACTACTGG ATTTCCTCAT AATTGACAAA CATGAGTGAC CACCTCTTTG GGTGGCTACT1440 GTTAGAAATG GCTGTTGTCA TGTTTTCTGG ACTTTGCCAG CCAACAGATC CCTGCCAGGT1500 TTTGGAAATA CTTCTATTAC CTCGCTGCTA CTTTTCTGCA GGGATAAAAC TTTTGNAGGT1560 GGCCAGACCC AGAACATCCA AGGATTCCTG TTACAGTGCT ACAGTATACA CTGCTCATTT1620 ATCCTATTCT CATGTGCTTT CTTCTTTAGT AAGATTATTT TAAGAAAATA AGTGATATTT1680 AAAGTCCAAA GAGGAATGAT CACAGTTGTA TAAGGGGTGT TTTCCCACTT GAACTCTGAT1740 GTCAGTCGAC TGTGGGTCAG AGCTACAACC ATCTGTTTGG TTTGATGTTT TGGTGGTTTA1800 CTTACGGAGT GGGGATAGTG TGAGACCTAA TTCCCTGTGC AAATGTCTCT TATTCCAGAA1860 ATGTGCATTT TGTCATCTAT AAGCAAGAAA TATGGGCATA GCAGCTCTTG GTTTAAANGT1920 TTGCCATAAC CTGTTCATGT TTGTTTTAAG CTCAGGTAAA GATAACCTCC NTCTTTCTAT1980 GACTCCAGTT TCCATTCAGG TTATAGTATT ATTCAATAGT TGATTTTCTT TTTAAGCTNG2040 GGCAATAAAT TGATGTTTCC AGATGGTAAC ATGGGANGAG GGCATATAGG ATAAAGATNG2100 AGCAAATTCT ACCCTAAAAA TGNTTCTAGT AGTTCACAGG AAGAAGATGA GGTTTAATAA2160 CTTTCAAGGT AATTCTAGAT TGACATTTTN GAGGGGAAAA TGGGCTCTTG TTCTAGTTGA2220 AGTGAGCAGA GAANGGCTAT NAAATTAATA TGTAANCTTA CAGCATTCCA GAGGTTAAAA2280 ATAACTGATG CAGATGTACT TCTTCAGTGT GATTCTTCAG ATCAAACTTT TACTTTTGGC2340 ATAGTTAATT TCAGAAAAAT GTGCTGTATG TGTGTGTGTA TGAGGGTTGG TCTTGCTGAT2400 CCTTCAGTTA GCTCTAAATT CTGGCAACTC CTTGTAATTC CCATGTATTT GATACCATGA2460 -----

### (2) INFORMATION ON SEQ ID NO. 611:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
    - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

TTTTTTTTT ATTTAAAGCC TGGATTGTAA CCAGATTTC TTTTTCCCC CTTCCAGCT 60
GTAGATATGA TATCTCCTTT CAGGGCCCCA GCTTAAGGGC AAAGTGAGTT AATGTGTAGA120
CAAAGGCGAG GGACAAGAG GAGTTAACAT CTAGACAGTG GAAAAAGCCA TGGTGTGTG180
TTTCTGGGAA CCACCAACAC TTGCAGGTTT AGCTTTTCC CAGGGTTGAC TACAAGAAAG240
AAAACCATGT TTTTGCAAGA TTAAAATGTG GTTGAGTGT CCTAAATTAA CCATCCCCAT300
TTTTATCATA TTTCCACCAT CACTTCAGGG TTTTAAGAGT CAGTGCTCAC CTGGGCGGAG360
CTGGTAGTAC ATTTTGCTTC TTAGAAAGCT AAGTCCTGGG TTCCGTCTGA TTTTAGGTTC420
CAGGAACTTC CTGAGAACAC CCGATCGCAG AGGGTAATTT TCTGGAGTTT GTTTTGCAGG480
GAAAGCAGCGC TTGCAGATGT ACAACTCGCA GCACCGGTCA ATGAATCAG CAGAAGTGGT540
GAAGCAGCGC TTGCAGATGT ACAACTCGCA GCACCGGTCA GCAATCAGCT GCATCCGGAC600
GGTGTGGAGG ACCGAGGGGT TGGGGGCCTT CTACCGGAGC TACACCACGC CAGCTGACCA660
TGAACATCCC CTTCCAGTCC ATCCACTTCA TCACCTATGA GTTCCTGCAG GAGCAGGTCA720
ACCCCCACCG GACCTACAAC CCGCAGTCCC ACATCATCT AGGCGGGCTG GCCGGGGCCC780
TTGCCGCGGC GGCGGGCC CCCCTGGACC TTTTAAGA 818

- (2) INFORMATION ON SEQ ID NO. 612:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1024 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

GCGGTCGGTA GTGCGGCGCT GTTTAAAGAT GGCGGCGGAG GAACCTCAGC AGCAGAAGCA 60 GGAGCCGCTG GGCAGCGACT CCGAAGTGTT AACTGTCTGG CCTATGATGA AGCCATCATG 120 GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCAGAGCGG 180 CTGGAGCTCT CGGTCCTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240 ATCAAGGACC TCCACAAAAA GTACTCGTAC ATCCGCAAGA CCAGGCCTGA CGGCAACTGT 300 TTCTATCGGG CTTTCGGATT CTCCCACTTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360 CAGCGGTTCA AGGCTGTGTC TGCCAAGAGC AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420 GAATTCACAA TTGAGGATTT CCACAACACG TTCATGGACC TGATTGAGCA GGTGGAGAAG 480 CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCAATGACC AGAGCACCTC CGACTACCTT 540 GTGGTCTACC TGCGGCTGCT CACCTCGGGC TACCTGCAGC GCGAGAGCAA GTTCTTCGAG 600 CACTICATCG AGGGTGGACG GACTGTCAAG GAGTTCTGCC AGCAGGAGGT GGAGCCCATG 660 TGCAAGGAGA GCGACCACAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720 CAGGTGGAGT ACATGGACCG CGGCGAGGGC GGCACCACCA ATCCGCACAT CTTCCCTGAG 780 GGCTCCGAGC CCAAGGTCTA CCTTCTCTAC CGGCCTGGAC ACTACGATAT CCTCTACAAA 840 TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCT CTGCCAGGCG CTAGACATGT 900 ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTCACC CCCTTCTTCC TGTCACATGA 960 

### (2) INFORMATION ON SEQ ID NO. 613:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1322 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

GCTGACCACG	ACATGTGTCT	CCTCCTCTGC	ACCTTCCAAG	ACCTCCTTAA	TAATGAACCC	60
	ACCAATGGAC	AGCTCTCAGT	CCACACTCCC	AAAAGGGAAA	GTTTGTCCCA	120
	CCCCATAGCC	ATCCTCTCTA	TGGACATGGT	GTATGCAAGT	GGCCAGGCTG	180
TGAAGCAGTG	TGCGAAGATT	TCCAATCATT	TCTAAAACAT	CTCAACAGTG	•	240
GGACGATAGA	AGTACAGCCC	AATGTAGAGT	ACAAATGCAG	GTTGTACAGC	AGTTAGAGCT	300
ACAGCTTGCA	AAAGACAAAG	AGCGCCTGCA	AGCCATGATG	ACCCACCTGC	ATGTGAAGTC	360
TACAGAACCC	AAAGCCGCCC	CTCAGCCCTT	GAATCTGGTA	TCAAGTGTCA	CTCTCTCCAA	420
GTCCGCATCG	GAGGCTTCTC	CACAGAGCTT	ACCTCATACT	CCAACGACCC	CAACCGCCCC	480
CCTGACTCCC	GTCACCCAAG	GCCCCTCTGT	CATCACAACC	ACCAGCATGC	ACACGGTGGG	540
ACCCATCCGC	AGGCGGTACT	CAGACAAATA	CAACGTGCCC	ATTTCGTCAG	CAGATATTGC	600
GCAGAACCAA	GAATTTTATA	AGAACGCAGA	AGTTAGACCA	CCATTTACAT	ATGCATCTTT	660
AATTAGGCAG			AAAGCAGCTA		AGATCTATAA	720
CTGGTTCACA	CGAATGTTTG	CTTACTTCCG	ACGCAACGCG	GCCACGTGGA	AGAATGCAGT	780
GCGTCATAAT	CTTAGTCTTC	ACAAGTGTTT	TGTGCGAGTA	GAAAACGTTA	AAGGGGCAGT	840
ATGGACAGTG	GATGAAGTAG	AATTCCAAAA	ACGAAGGCCA	CAAAAGATCA	GTGGTAACCC	900-
TTCCCTTATT	AAAAACATGC	AGAGCAGCCA	CGCCTACTGC	ACACCTCTCA	ATGCAGCTTT	960
ACAGGCTTCA	ATGGCTGAGA	ATAGTATACC	TCTATACACT	ACCGCTTCCA	TGGGAAATCC1	.020
CACTCTGGGC	AACTTAGCCA	GCGCAATACG	GGAAGAGCTG	AACGGGGCAA	TGGAGCATACI	080
CAACAGCAAC	GAGAGTGACA	GCAGTCCAGG	CAGATCTCCT	ATGCAAGCCG	TGCATCCTGTI	140
ACACGTCAAA		TCGATCCAGA	GGAAGCTGAA	GGGCCCCTGT	CCTTAGTGACI	200
AACAGCCAAC		ATTTTGACCA		`	AACCAGTAAAI	260
CGAGGACATG	0		CAACCCCGAG	AATGAAGATT	GGAAAAAGGA1	320
AA	J J J				1	322

### (2) INFORMATION ON SEQ ID NO. 614:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 4458 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

			•			~ ^
GCCCGGCGTT	AACAAAGGGA	GCCGATACCG	ACCGGCGTGG	GCGCGGAGCG	GGCGGCCGCC	60
ACCGAGCGTG	CTGAGCAACC	GCAGCCTCCG	CGGCCGAGAG	TGCAGCGAGC	AAGGGGACAA	120
ARRECCCC	AAACCCCCCA	CAACCAGCAC	CACAGAGAGA	AGGGAAGAAC	GGCATCCAGC	180
AAAGIICCGC	AAAGCCCGCA	CALCONOCIC	TCTCCAAACC	CCGCAGCACA	CGTGACCATA	240
CCACCAGAAA	TGGACCGACA	CACCICAGCA	ICICCAAACC	CCGCAGCACA		200
AACCAGCAAA	GATGAGTTTT	GATCATCCTG	AGAAAAATGG	GCCTTGGCCT	GCAGACCCAA	300
TANACCTTCC	CTCCCATGGA	TAATAGTGCT	AATTCCTGAG	GACCTGAAGG	GCCTGCCGCC	360
IMMCCIICC	C1CCC			CAACAAACTC	A CTTTCCCTGA	420
CCTGGGGGAT	TAGCCAGAAG	CAGGCTTGTT	TICCIGCICA	GAACAAAGIG	ACTTCCCTGA	720
ACACATOTTO	ATTATGATTC	ACACCAACCT	GAAGAAAAAG	TTCAGCTGCT	GCGTCCTGGT	480
ACACATOTIC	MMMCC3 CTC3	TOTOTOTOTO	CAACCAAAAC	AAGAAAGGGA	GTTACTATGA	540
CTTTCTTCTG	TITIGCAGICA	101919191	Granderatio		* * * * * * * * * * * * * * * * * * *	600
TTCCTTTAAA	TTGCAAACCA	AGGAATTCCA	GGTGTTAAAG	AGTCTGGGGA	AATTGGCCAT	600
	macan amama	TATCCTCAAC	CACCACCCAG	GACCCCCACA	GGGGCCGCCA	660
GGGGTCTGAT	TCCCAGTCIG	IMICCICAMG	CAGCACCCIA		TOOL COMONG	720
GACCCTCGGC	AGTCTCAGAG	GCCTAGCCAA	GGCCAAACCA	GAGGCCTCCT	TCCAGGTGTG	120
	N.C.C.C.C.C.C.C.A	AAAACCTTAT	CCCTAGGCTG	CAAAAGATCT	GGAAGAATTA	780
GAACAAGGAC	AGCICITCOM	WWW.CC! IVI	00011100010			

CCTAAGCATG AACAAGTACA AAGTGTCCTA CAAGGGGCCA GGACCAGGCA TCAAGTTCAG 840 TGCAGAGGCC CTGCGCTGCC ACCTCCGGGA CCATGTGAAT GTATCCATGG TAGAGGTCAC 900 AGATTTTCCC TTCAATACCT CTGAATGGGA GGGTTATCTG CCCAAGGAGA GCATTAGGAC 960 CAAGGCTGGG CCTTGGGGCA GGTGTGCTGT TGTGTCGTCA GCGGGATCTC TGAAGTCCTC1020 CCAACTAGGC AGAGAAATCG ATGATCATGA CGCAGTCCTG AGGTTTAATG GGGCACCCAC1080 AGCCAACTTC CAACAAGATG TGGGCACAAA AACTACCATT CGCCTGATGA ACTCTCAGTT1140 GGTTACCACA GAGAAGCGCT TCCTCAAAGA CAGTTTGTAC AATGAAGGAA TCCTAATTGT1200 ATGGGACCCA TCTGTATACC ACTCAGATAT CCCAAAGTGG TACCAGAATC CGGATTATAA1260 TTTCTTTAAC AACTACAAGA CTTATCGTAA GCTGCACCCC AATCAGCCCT TTTACATCCT1320 CAAGCCCCAG ATGCCTTGGG AGCTATGGGA CATTCTTCAA GAAATCTCCC CAGAAGAGAT1380 TCAGCCAAAC CCCCCATCCT CTGGGATGCT TGGTATCATC ATCATGATGA CGCTGTGTGA1440 CCAGGTGGAT ATTTATGAGT CCCTCCCATC CAAGCGCAAG ACTGACGTGT GCTACTACTA1500 CCAGAAGTTC TTCGATAGTG CCTGCACGAT GGGTGCCTAC CACCCGCTGC TCTATGAGAA1560 GAATTTGGTG AAGCATCTCA ACCAGGGCAC AGATGAGGAC ATCTACCTGC TTGGAAAAGC1620 CACACTGCCT GGCTTCCGGA CCATTCACTG CTAAGCACAG GCTCCTCACT CTTCTCCATC1680 AGGCATTAAA TGAATGGTCT CTTGGCCACC CCAGCCTGGG AAGAACATTT TCCTGAACAA1740 TTCCAGCCTG CTCCTTTTAC TCTAGGGGCC TCTGTCAGCA AGACCATGGG GACTTCAAGA1800 GCCTGTGGTC AGGAAATCAG GTCCAGCCTT CCCTGTAGCC AGACAGTTTA TGAGCCCAGA1860 GCCTCCTGCC ACACACATGC ACACATATCT AGCATTCTTT CCAGACAGCA TCCTCCCGC1920 CTTCCACCTT GGTAGATGCA AGGTCTATCT CTCCCATCAG GGCTGCCAAA GCTGGGCTTT1980 GTTTTTCCCA GCAGAATGAT GCCATTCTCA CAAACCAATG CTCTATATTG CTTNGAAGTC2040 TGCATCTAAA TATTGATTTC ACGNTTTTAA AGNAAATTCT NNCTTAAATT ACAATTGTGC2100 CCAATGCAGG GTGGNCTCTN NGGGGGGCAA GTAGGTGGTA CAGGGGATTG GAAACATCCT2160 CCGCGCCTCC AGAGAAAAGT TGCTCCCGAG GTCCATGCCC CTGGAACGTG TTCCTATCAC2220 TCTGGCTGGT TGGGCTGGTC CTTAGACTGG GTGCTTATGA TTAAAAGGGT CTTGGTTAAG2280 CCCACTTTCC CTCTCCATGT GGAGATGGAA GGTAGAGAAG GATACAGTGT CTATCCTCAA2340 GTTGCTACGG TTCAGTGAGA GAGGCAGACA TCTGAACAGG NCAGGTAGGA TTCAGTGTGC2400 TCAGTGCACT GGGGATTTGG AGAGAGATGG GCTTGCTCTC TCTGTGCACC CAGGAGGGCC2460 ACGCACTTAA AACTGTGTTT GTGGATCAGA GAAGGCTTTA TAGCACAGGG GGCATTCAGA2520 TGAGTCTTAG AGGAAGAGA GAAACATGGC AAGCAGATTA CATCTGAGCC GTTTGAATTG2580 TGTTTTCTT TCTTCCCATG TTTATTTCT AAGATCTACC TGAACTTAGN AGACTCAAGA2640 TATTTTTTTA GGAAACCTCC TACCCATGTC TGAGGTAGCA AGTGCAGCCT CACGACAGAT2700 ACCAGGCAAT CCAGAGCCAC AAAACGTGAT TCCTCCAGGC TCTGCCTGGC CTGACCCTGT2760 CCTGTCAGCT GGGTTTACAT ACCAGTCCCA TTCTTCCTTT TCAATACCTA CCCCCAAATC2820 TTCTCCTAAC CACCATCTGT TTTTTTTAG TTAAAGCATT TTTTGCTTTA AAAGCATCCT2880 GACCCCAATT TCTTTGAGCT CACGGGCCTT TTGCTGAAGG TCTCTCAGGG TGTAGTGGTG2940 TGGCTCTCTG GACTTAACGT CACTCTCAGN AGGTCAGAAC CTTNGGAGAT CAGAACTGAT3000 TCTCACCAGG TGTGAGAGGT GTGGNTANGC AGATTGCAAT GCTCTGCACC TCTTNCCTTG3060 CAAGTGAGNC AACTTNCAGG NCTCTCTGGG NCAGAGGCTG GCCCACTGTA GTTTGCAGAC3120 ATGCTCTCCA GATGGNTTTT ACTAAGTCCC CTCTCCCTGN ATANGGGAAT CCTGNCTGGN3180 ACCAGCGCAN GCCCTNNGGT GTNGGANNGA GGTTNAAAAG ACTTGNCACA GGNATCACCA3240 AGTNCATGCT GNTAGANGCC AGGATTCCTA GACCCAGGGC TCTGCACTCT CAAGGCTGGC3300 CCCATGTGCT CAAGGGGGTC TAATGTTTGG GCTCCAAACT AACCATCTCG GAGCTGGGCT3360 CCTCATTTAC TGCCAAACCC TCAGNCTTAT GTAGCNTAGA AAGGGCCCTG GANGTGNAGA3420 AAGCCTGGAT TTTCAAATTG ATGCTCCCCT ACTNGACTAG NCTGTGCCAC TCNTGGGCAA3480 ATGCTCTTCC TTGAGCCTGT TTCCACACCT GTAAAGTGGG GATGATGATC CTATCTCACT3540 GCTTTTNGTG NAGGATTACA GGNNAAAGCA CCTGTCCTGG CTCTGTACCT GGCACGTAGT3600 ANGGTGCTCA GTTCATGCTG GTTTCCTTCC TGCCTTTAGT AGGGACCTGC TCTGTGCTCA3660 CACCTCGGCT GCATGCACCC TGCTGTGACG GAGGCTAGTG TGGAAGAGGT CCTGTCCTCA3720 GGGAATTAAC TGTCTTATTG GGAGACAACA ACTGTCCTCC TTGGAACACC CAAGAAACCA3780 TGNCAAAGCA GTGGACAACA CAGAACACGN CCCTCCTCCT CGCTGCCTGC AGCTNCCAAT3840 CTGATTCTGC TTGGGAATGG GCGGANCACG NTGGGCTGCT TAACTGCTGT ATAGGACAAG3900 CCCCTTACCC CTCTCTGGGC CCATGAATTC CTGGCTTGGT TTATGTTCTG ATTTGACACA3960 CTGATTTTAA TCTTCGAATC ATGACACTGA GTGCAGAGGA GGTGGCATTC CGACAGCAGG4020 ACATACATGT TNGGTGTGAA GACTGGGACG ACACTGGGTA GAATCTAGTT TTTAATTATT4080 ATTAATATAA AGGATCAAAT TAATTTAAAT ATGAATCTGA AGTCCACAGA ACTTTNNNNN4140 AAGTGCTGTC CAGGCCAACA CTTTGGTAAA ATGCAAATTA TGATATGGAC GTTATCATTG4200 GTCTGGTGAG ATGTTTCATA TTTGTGACAG TTAATTTAAA AATTATGACT TAATGCTGCC4260 TGTGTCTATG GGGTTCTGTC TTCTTTGATA GCCATCTATT CATCTGGATC ATGGGACCCT4320 CTCTAATCCT TCCACCAATC AAATAAGCTA TTGCTATTGG TTTGGAGTTG AGATATCAGT4380 CTCGGAAACT TCTGAAAAAT GCTAATAATT ACCCAAGGAT TATGTCAAAT TTTAAAATAA4440 ATGTGTGTGT GTTTCTTT

- (2) INFORMATION ON SEQ ID NO. 615:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1562 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TGGAGGCAGC TAGCGCGAGG GTGGGGAGCG CTGAGCCGCG CGTCGTGCCC TGCGCTGCCC 60 AGACTAGCGA ACAATACAGT CAGGATGGCT AAAGGTGACC CCAAGAAACC AAAGGGCAAG 120 ATGTCCGCTT ATGCCTTCTT TGTGCAGACA TGCAGAGAAG AACATAAGAA GAAAAACCCA 180 GAGGTCCCTG TCAATTTTGC GGAATTTTCC AAGAAGTGCT CTGAGAGGTG GAAGACGATG 240 TCCGGGAAAG AGAAATCTAA ATTTGATGAA ATGGCAAAGG CAGATAAAGT GCGCTATGAT 300 CGGGAAATGA AGGATTATGG ACCAGCTAAG GGAGGCAAGA AGAAGAAGGA TCCTAATGCT 360 CCCAAAAGGC CACCGTCTGG ATTCTTCCTG TTCTGTTCAG AATTCCGCCC CAAGATCAAA 420 TCCACAAACC CCGGCATCTC TATTGGAGAC GTGGCAAAAA AGCTGGGTGA GATGTGGAAT 480 AACTTAAATG ACAGTGAAAA GCAGCCTTAC ATCACTAAGA CGGCAAAGCT GAAGGAGAAG 540 TACGAGAAGG ATGTTGCTGA CTATAAGTCG AAAGGAAAGT TTGATGGTGC AAAGGGTCCT 600 GCTAAAGTTG CCCGGAAAAA GGTGGAAGAG GAAGATGAAG AAGACGGGGG GGGGGGGGG 660 GGGGGGGGG GGGGGACGTA TAGTCGGGTC GGCTGGTGGA GTAGCCCAAA AGAAGGGGAG 720 CGCCGTAATT GACACATCTC TTATTTGAGA AGTGTCTGTT GCCCTCATTA GGTTTAATTA 780 CAAAATTTGA TCACGATCAT ATTGTAGTCT CTCAAAGTGC TCTAGAAATT GTCAGTGGTT 840 TACATGAAGT GGCCATGGGT GTCTGGAGCA CCCTGAAACT GTATCAAAGT TGTACATATT 900 TCCAAACATT TTTAAAATGA AAAGGCACTC TCGTGTTCTC CTCACTCTGT GCACTTTGCT 960 GTTGGTGTGA CAAGGCATTT AAAGATGTTT CTGGCATTTT CTTTTTATTT GTAAGGTGGT1020 GGTAACTATG GTTATTGGCT AGAAATCCTG AGTTTTCAAC TGTATATATC TATAGTTTGT1080 AAAAAGAACA AAACAACCGA GACAAACCCT TGATGCTCCT TGCTCGGCGT TGAGGCTGTG1140 GGGAAGATGC CTTTTGGGAG AGGCTGTAGC TCAGGGCGTG CACTGTGAGG CTGGACCTGT1200 TGACTCTGCA GGGGGCATCC ATTTAGCTTC AGGTTGTCTT GTTTCTGTAT ATAGTGACAT1260 AGCATTCTGC TGCCATCTTA GCTGTGGACA AAGGGGGGTC AGCTGGCATG AGAATATTTT1320 TTTTTTTAAG TGCGGTAGTT TTTAAACTGT TTGTTTTTAA ACAAACTATA GAACTCTTCA1380 TTGTCAGCAA AGCAAAGAGT CACTGCATCA ATGAAAGTTC AAGAACCTCC TGTACTTAAA1440 CACGATTCGC AACGTTCTGT TATTTTTTT GTATGTTTAG AATGCTGAAA TGTTTTTGAA1500 1562 AA

#### (2) INFORMATION ON SEQ ID NO. 616:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2278 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

GGCAATTTCC GTTAGGTGCT GAAGGCTGTG GCGCGCGGCT GTCCCCATTC CCACGTGAAG 60 CGCTACGCTA GCATCGCTCG GCTGGCGGCT CCCAGCTCGC CGCGGAGCAG TCCCGGCAGC 120 AGCGGGGGAC CGGAAGTGGC TCGCGGAGGC TCAGAAGCTA GTCCCGGAGC CCGGCGTGTG 180 GCGCCTCGGA GCACGGTGAC GGCGCCATGT CCCTAATCTG CTCCATCTCT AACGAAATGC 240 CGGAGCACCC ATGTGTATCC CCTGTCTCTA ATCATGTTTA TGAGCGGCGG CTCATCGAGA 300 AGTACATTGC GGAGAATGGT ACCGACCCCA TCAACAACCA GCCTCTCTCC GAGGAGCAGC 360 TCATCGACAT CAAAGTTGCT CACCCAATCC GGCCCAAGCC TCCCTCAGCC ACCAGCATCC 420 CGGCCATTCT GAAAGCTTTG CAGGATGAGT GGGATGCAGT CATGCTGCAC AGCTTCACTC 480 TGCGCCAGAG CTGCAGACAA CCCGCCAAGA GCTGTCACAC GCTCTGTACC AGCACGATGC 540 CGCCTGCCGT GTCATTGCCC GTCTCACCAA GGAAGTCACT GCTGCCCGAG AAGCTCTGGC 600 TACCCTGAAA CCACAGGCTG GCCTCATTGT GCCCCAGGCT GTGCCAAGTT CCCAACCAAG 660 TGTTGTGGGT GCGGGTGAGC CAATGGATTT GGGTGAGCTG GTGGGAATGA CCCCAGAGAT 720 TATTCAGAAG CTTCAAGACA AAGCCACTGT GCTAACCACG GAGCGCAAGA AGAGAGGGAA 780 GACTGTGCCT GAGGAGCTGG TGAAGCCAGA AGAGCTCAGC AAATACCGGC AGGTGGCATC 840 CCACGTGGGG TTGCACAGTG CCAGCATTCC TGGGATCCTG GCCCTGGACC TCTGCCCGTC 900 CGACACCAAC AAGATCCTCA CTGGTGGGGC GGATAAAAAT GTCGTTGTGT TTGACAAAAG 960 TTCTGAACAA ATCCTGGCTA CCCTCAAAGG CCATACCAAG AAGGTCACCA GCGTGGTGTT1020 TCACCCTTCC CAGGACCTGG TGTTTTCTGC TTCCCCCGAT GCCACTATCA GGATTTGGTC1080 GGTCCCCAAT GCCTCTTGTG TACAGGTGGT TCGGGCCCAT GAGAGTGCTG TGACAGGCCT1140 CAGCCTTCAT GCCACTGGCG ACTATCTCCT GAGCTCCTCC GATGATCAGT ACTGGGCTTT1200 CTCTGACATC CAGACAGGGC GTGTGCTCAC CAAGGTGACA GATGAGACCT CCGGCTGCTC1260 TCTCACCTGT GCACAGTTCC ACCCTGACGG ACTCATCTTT GGAACAGGAA CCATGGACTC1320 TCAGATCAAG ATCTGGGACT TGAAGGAACG TACTAATGTG GCCAACTTCC CTGGCCACTC1380 GGGCCCCATC ACTAGCATCG CCTTCTCTGA GAATGGTTAC TACCTGGCTA CAGCGGCTGA1440 TGACTCCTCT GTCAAGCTCT GGGATCTGCG CAAGTTAAGA ACTTTAAGAC TTTGCAGCTG1500 GATAACAACT TTGAGGTAAA GTCACTGATC TTTGACCAGA GTGGTACCTA CCTGGCTCTT1560 GGGGGCACGG ATGTCCAGAT CTACATCTGC AAACAATGGA CGGAGATTCT TCACTTTACA1620 GAGCATAGCG GCCTGACCAC AGGGGTGGCC TTCGGGCATC ACGCCAAGTT CATCGCTTCA1680 ACAGGCATGG ACAGAAGCCT CAAGTTCTAC AGCCTGTAGG CCCTGGCCCT TCTGATGGAA1740 GCTGGGCCTC ATCTCAGTAG AGGGGTAGAA TTAGGGTTTG GGGGGGGGTG GGGGGAATCT1800 ATGGGGGGAG GGGGCTCTGT GGGGTGGGAC ATTCACATCA TTTCACTCTG GTCTGAGTGG1860 TGGCCTGAGA ACCATGGTGG CATGGACCAC CCTCATCCAT GCAACTCCAG GCCCCATGGG1920 AACGGATGTG GAAGGAAGAA CTGTCACCCT CTTAAGGCCC AGGGTCGGAG CCCAGGGCCT1980 CTCCCTTCCT GTCGTTCAAT GGACGTGGTG GTGGCTGTTC CACACCCATT TTGTTGCAGT2040 TCCTGTGAGA CAGGAGAGGC TGAGCCAAGG GAACTGTGAA GGGGATGGGC AGGAGGGCTT2100 GTGCAGGGTT TTGTAAGCAG TGATCTAGTT TCATTAAAAA AAGAAAACAA TAACCATAAC2160 CACCTCCCCG TGTCTGTCTG CACCAGGAGC ACCTGGGACT GGGAAGTCAA GGGGAGGGAG2220 CACACACTGG GACACTGGCT TCCGGGAAGC CCATCTTCCT TTCCTTTCAC AGCTCTTA

- (2) INFORMATION ON SEQ ID NO. 617:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 931 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

CAGGGGCGTG CAGCCCGCTT GCCAATCAGA GCGCGGCTGA GCGGCCCCGC AGCCAACCCC 60 CGAGGAGCGG CCGGCTGGCG TCCGCCGCGC CCAGGAGTTG GGGATGTCCT ACAAACCCAT120 CGCCCTGCT CCCAGCAGCA CCCCTGGCTC CAGCACCCCT GGGCCGGGCA CCCCGGTCCC180 TACAGGAAGC GTCCGTCGC CGTCGGGCTC AGTGCCAGGA GCCGGCGCTC CTTTCAGACC240 GCTGTTTAAC GACTTTGGAC CGCCTTCCAT GGGCTACGTG CAGGCGATGA AGCCACCCGG300 CGCCCAGGGC TCCCAGAGCA CCTACACGGA CCTGCTGTCA GTCATAGAGG AGATGGGCAA360 AGAGATCCGG CCTACCTATG CTGGCAGCAA GAGCGCCATG GAGCGCCTGA AGAGAGGTAT420 CATCCATGCC CGGGCCCTAG TCAGAGAGTG CCTGGCAGAG ACAGAGCGGA ACGCCCGCAC480 GTAACAGGAA GCGCCTCGGC CTCAGCGTCT GGACCTATCC GGCCACTGCA GAGCACCCGC540 TTCTCCCTGG CCTTCATCCC GAGTTGCACT AACCATCCTG GGCTTCCTGT CCTGTGTCCC600 TTGGTGGGTC CCCTCCAGGA ACCAAGGAGT GGCCCTCCAG GTGGCAGCAC TAAGGACACC660 CCCCCACAAC AAGAGTTAGC AGCGAGGTCC CCATGAGTCC CACCCATGAC CTGCCGACAG720 TGTTGCCCAC CGGAACTTTT GTGGCCCCTA CCGCTCAGCC CTTCCCAGCA CTTCTCCCAC780 TTTGTCCCGA GCCTCCTTCT CGCCCAGCAG GGGCACAGGC CTGGCACCTC CCTGCCTTGT840 GTCCTGAGCC ATAGTGACTC TTTTATCTGT GTGTCTTTTG CTAAATATGC CCTTTTTATA900 TTAATAAAAG ATGATTTGGA GTTGTGCTCT C

- (2) INFORMATION ON SEQ ID NO. 618:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 447 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

ELPSSPPPGL PEVAPDATST GLPDTPAAPE TSTNYPVECT EGSAGPQSLP LPILEPVKNP 60
CSVKDQTPLQ LSVEDTTSPN TKPCPPTPTT PETWGGGGGG APSSTPCSAH LTPSSLFPSS120
LESSSEQKFY NFVILHARAD EHIALRVREK LEALGVPDGA TFCEDFQVPG RGELSCLQDA180
IDHSAFIILL LTSNFDCRLS LHQVNQAMMS NLTRQGSPDC VIPFLPLESS PAQLSSDTAS240
LLSGLVRLDE HSQIFARKVA NTFKPHRLQA RKAMWRKEQD TRALREQSQH LDGERMQAAA300
LNAAYSAYLQ SYLSYQAQME QLQVAFGSHM SFGTGAPYGV RMPFGGQGPL GAPPPFPTWP360
GCPQPPPLHA WQAGTPPPPS PQPAAFPQSL PFPQSPAFPT ASPAPPQSPG LQPLIIHHAQ420
MVQLGLNNHM WNQRGSQAPE DKTQEAE

- (2) INFORMATION ON SEQ ID NO. 619:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 205 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ADAGGGTERS LLSLPPELLV LPGTDGAAPG GFWEPHVIWD WGALWGQNAL WGPGAPGSPA 60 TLSHLAGVPA AATPARMAGW HPPTALPTAS SLSTVTALPA VPSLPYGLTR TPSEPRAATP120 HYPPRTDGTA GAEQPHVEPE RVPGARGQDA GGRMTACPCL TTWGTPLDPG IGQDPIEHPG180 LPCALWTVED EVICHFQDIV REPFI 205

- (2) INFORMATION ON SEQ ID NO. 620:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 409 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

KSRLSVTLMP VQLSEHPEWN ESMHSLRISV GGLPVLASMT KAADPRFRPR WKVILTFFVG 60
AAILWLLCSH RPAPGRPPTH NAHNWRLGQA PANWYNDTYP LSPPQRTPAG IRYRIAVIAD120
LDTEPTAQDE NTWRSDLKKG YLTLSDSGDK VAVEWDKDHG VLESHLAEKG RGMELSDLIV180
FNGKLYSVDD RTGVVYQIEG SKAVPWVILS DGDGTVEKGF KAEWLAVKDE RLYVGGLGKE240
WTTTTGDVVN ENPEWVKVVG YKGSVDHENW VSNYNALRAA AGIQPPANLI HESACWSDTL300
QRWFFLPRRA SQERYSEKDD ERKGANLLLS ASPDFGDIAV SHVGAVVPTH GFSSFKFIPN360
TDDQIIVALK SEEDSGRVAS YIMAFTLDGR FLLPETKIGS VKYEGIEFI 409

- (2) INFORMATION ON SEQ ID NO. 621:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 249 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

KLSPDGLAQC FRFELNELDA FVFHASDLGL RQQEAPVQRE GHDVGGDSAA VLLGFEGHND 60 LVVGVGDELE GREAVSGDHR PDVAHSDVAE VRGGAQQQVG ALALVVLLAV ALLAGAARQE120 EPALQRVTPA GRLMDEVSWR LDAGSSPQGV VVGHPVLVVH AALVAHHLHP LRVLVHHITR180 SGRPLLAQAA HVQTLVLHCQ PFGLEAFLHG AVAVGQNHPG HGFAAFDLVD DPRPVIHGVE240 FPIENNQVG 249

- (2) INFORMATION ON SEQ ID NO. 622:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 255 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AAAPVSLHDA AGDLRRDPGG GGGGGVPHGG GEGQEVVPAE PGVPAPQHAE PVAAAGAAQQ 60 LQTEEQPGLQ RLRLGPVRGA ARGGDARVRG PRGDRRVNPE SARALLPGDP QGPGTAAPRA120 LGLPPRCEPV GAPLAALALA RERRERGRFP RPCKCLFFNS SQCELCCECV RGGAPALSRR180

RVATPCPCPM VCNSDFAHRS TVPPSAHPFT LTPTLSLNTF IIVRRGRWDF GRSAAATASG240 GLIFIFALRW LKAFI 255

- (2) INFORMATION ON SEQ ID NO. 623:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 196 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIIKVFSE SVGVSVNGCA LGGTVERCAK 60 SELQTIGQGH GVATRRRLSA GAPPRTHSQQ SSHWEELKNK HLQGRGKRPR SRRSRARASA120 ARGAPTGSQR GGSPSARGAA VPGPCGSPGS RARALSGFTR RSPRGPRTRA SPPRAAPLTG180 PSRSRWSPGC SSVCSC

- (2) INFORMATION ON SEQ ID NO. 624:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 242 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

VESHRRAHTH TTVRSPETAR GWKPWPHRLS RYVHSPGRQP HGHGQHLCFC SGRRAFGGHP 60 RQGARASLLA LGLENSPGGS SPEERLGRLA VAGPPRGAQN VSQAGPEAEA PPLRFGHAWG120 AQTPRLGAPG PWTPLPTLPS HIPPFWSQTP AQRKEGFTEE GQGRAWPQGG DEDISGPGSC180 RLLWEEEPCV CKLLGLAARP TAGPSLDPCT WPSSCPLAAP GLGTGIEPRG LGWLGQGRDR240 EG 242

- (2) INFORMATION ON SEQ ID NO. 625:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 216 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSQRKARA EPGPREGMRT 60 FPVQVAAGCS GRKSHASVNC WGWRPAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120 WARAGTGRGS TSDPDVGWLC PPRREAQQTS YTKAKSTIGE PRSHFMGRRP RPQGPQSKAR180 GRFIPEDSPP GAAPAWGGVS RPLGCLSVCG TPWSTP

- (2) INFORMATION ON SEQ ID NO. 626:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 299 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

PGISVSVDKM ESSPFNRRQW TSLSLRVTAK ELSLVNKNKS SAIVEIFSKY QKAAEETNME 60 KKRSNTENLS QHFRKGTLTV LKKKWENPGL GAESHTDSLR NSSTEIRHRA DHPPAEVTSH120 AASGAKADQE EQIHPRSRLR SPPEALVQGR YPHIKDGEDL KDHSTESKKM ENCLGESRHE180 VEKSEISENT DASGKIEKYN VPLNRLKMMF EKGEPTQTKI LRAQSRSASG RKISENSYSL240 DDLEIGPGQL SSSTFDSEKN ESRRNLELPR LSETSIKDRM AKYQAAVSKQ SSSPTIPMS 299

- (2) INFORMATION ON SEQ ID NO. 627:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

DSAPSPGFSH FFFNTVRVPF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLLT60 RESSLAVTLN DSEVHCRLLN GDDSILSTDT EIPG 94

- (2) INFORMATION ON SEQ ID NO. 628:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 765 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTPNFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEIVDWSK FDASSGEHEK CGQYIQKGYS180
KLKIYNCELE NVAEFEGLTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
ELSCYLPQEK DLKISVYDYD TFTRDEKVGE TIIDLENRFL SRFGSHCGIP360
EYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDGS RIRYGGRDYS LDEFEANKIL420
HQHLGAPEER LALHILRTQG LVPEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYYLRVIIWN TKDVILDEKS ITGEEMSDIY VKGWIPGNEE NKQKTDVHYRS40
SLDGEGNFNW RFVFPFDYLP AEQLCIVAKK EHFWSIDQTE FRIPPRLIIQ IWDNDKFSLD600
DYLGFLELDL RHTIIPAKSP EKCRLDMIPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
DGARVMAGKV VIIGLLFLLI LLLFVAVLLY SLPNYLSMKI VKPNV 765

# (2) INFORMATION ON SEQ ID NO. 629:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 289 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60 FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120 CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180 PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240 NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNFQVFFLR 289

#### (2) INFORMATION ON SEQ ID NO. 630:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 824 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

RVSVLAAASS ALPVAPREAG VTNWPAGCVP EVRSTGEKEV AKTLHRRSRP EWCGARDPPA 60
MLLFVLTCLL AVFPAISTKS PIFGPEEVNS VEGNSVSITC YYPPTSVNRH TRKYWCRQGA120
RGGCITLISS EGYVSKYAG RANLTNFPEN GTFVVNIAQL SQDDSGRYKC GLGINSRGLS180
FDVSLEVSQG PGLLNDTKVY TVDLGRTVTI NCPFKTENAQ KRKSLYKQIG LYPVLVIDSS240
GYVNPNYTGR IRLDIQGTGQ RLFSVVINQL RLSDAGGYLC QAGDDSNSNK KNADLQVLKP300
EPELVYEDLR GSVTFHCALG PEVANVAKFL CRQSSGENCD VVVNTLGKRA PAFEGRILLN360
PQDKDGSFSV VITGLRKEDA GRYLCGAHSD GQLQEGSPIQ AWQLFVNEES TIPRSPTVVK420
GVAGGSVAVL CPYNRKESKS IKYWCLWEGA QNGRCPLLVD SEGWVKAQYE GRLSLLEEPG480
NGTFTVILNQ LTSRDAGFYW CLTNGDTLWR TTVEIKIIEG EPNLKVPGNV TAVLGETLKV540
PCHFPCKFSS YEKYWCKWNN TGCQALPSQD EGPSKAFVNC DENSRLVSLT LNLVTRADEG600
WYWCGVKQGH FYGETAAVYV AVEERKAAGS RDVSLAKADA APDEKVLDSG FREIENKAIQ660
DPRLFAEEKA VADTRDQADG SRASVDSGSS EEQGGSSRAL VSTLVPLGLV LAVGAVAVGV720
ARARHKNVD RVSIRSYRTD ISMSDFENSR EFGANDNMGA SSITQETSLG GKEEFVATTE780
STTETKEPKK AKRSSKEEAE MAYKDFLLQS STVAAEAQDG PQEA

- (2) INFORMATION ON SEQ ID NO. 631:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 267 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

ADIAGPRCLP LFNCHIDGCS LSIEVALLHS TPVPALISPG HQVQGQGDKP AVLVTVHEGL 60
AGAFVLAGQG LAARVIPLAP VFLVRGEFAW KVTGDLESLS QHSRDIPWYL EVWFSFDNLD120
LHGGPPESIA VGQTPVEAGV PAGELVEDDS EGAVAWLLQQ GEAALVLGLN PPLAVHQQGA180
AAILGPFPET PVLDAFAFLT VVGAEHGHRA SCHPLHHSGA AGNRGLLIDE ELPGLDRRAF240
LQLTIRMGST QVAPCILLPQ ACDHTE

- (2) INFORMATION ON SEQ ID NO. 632:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRLPC 60 THLPWWAGFS LLGSTLPPSV HDTDPRASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120 GQKEVACGNL RSPHPRFPKR 140

- (2) INFORMATION ON SEQ ID NO. 633:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

  VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSGSSE SQEPRMRALC 60

  SPSSKTQGSP PRKGAHVPQR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120
  DLFSGCK
  - (2) INFORMATION ON SEQ ID NO. 634:
    - (i) SEQUENCE CHARACTERISTIC:
      - (A) LENGTH: 140 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

HHQKHMQGKG SYWASGLLSP WLGRKGREDG WGSLFGIDDV HEFGLEGSTT HKEAIHIRLA 60 GQLLAGCPSH RASINDTGAL SHRIRDVGLQ PSSELLVYFL GLLGCCSLAS TNGPHRLIGQ120 DDLAPVLHVI CDDLLVWWEG

- (2) INFORMATION ON SEQ ID NO. 635:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

KVIADNVKDW SKVVLAYEPV WAIGTGKTAT PQQAQEVHEK LRGWLKSNVS DAVAQSTRII 60 YGGSVTGATC KELASQPDVD GFLVGGASLK PEFVDIINAK Q 101

- (2) INFORMATION ON SEQ ID NO. 636:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 329 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

DSIFPLWAVL ALSPPGIRVR MKKSSVSGMT AAGWVVWGEA EGKAALRLGV EFLEVWGGGR 60 VFNLEKSQPA RAERECERGS SEGARNGVGG SGGRSVAVAL VHQHGVRLLG DLQQRVHVGA120 APAPQVAGLP PLRAALVVVG AHLHHLGGLE HFHLALADLL DVEGEGWHLV DRGLGARVHH180 VVGREGFAQL VPRRLQFLAP LGGHQARAQL VHALLQGVPR LLQVFLGLEA RLLQVLAGTH240 LGLLHLLLGE GLLEVVHAPQ ALRLIRSARD SSITSSTSTA SSDESSSAAA SSSGRSPSPS300 SSPSFSGSAS DSFSDLLMLS LAGSFTSSW 329

(2)	INFORMATION	ОИ	SEQ	ID	NO.	637:
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- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 263 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60 TQAQLEERQA EMEGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSLER120 QAGQIKKLEV NEAELLRRNN FKVMIYQDEV KLPAKLSISK SLKESEALPE KEGEELGEGE180 RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSRRPSPRRR WRRPRCVPAR240 TWRRRASRPR KTWRRRGTPW RSA

- (2) INFORMATION ON SEQ ID NO. 638:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 205 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

SGDLRLLVDT SKVQEAWVPS QDTHHTQELL AVQGSLVSGY RPGGGFGAAP VHEDPHLLGP 60
ASRGAPETAA FFFFFFFFP EQHLRVGLLL LPPRLSPRPG PAWPVPNPVG WPGHLHQGGQ 120
LLAGTNKPFH LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLXTPQQLXG PRXXFPXAVQ 180
ASPXPGVCSL AWVELCHIXD KQXGG 205

- (2) INFORMATION ON SEQ ID NO. 639:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

PVTPRDXPGA GGGSXEGPMQ HPGQSRPXPL AXPAPXWXLM APCGALTCWA RLXLGLSAPX 60 LLIXDVTELD PSQAAHSWTW ASLHCXGKXX PRAXKLLRGX EAGAHPQASV FSAPPCPRFR120 ASVHREHHHH GQVEGFISPC QQLSSLVQVA WPAHWIGDGP GWARSGAQSG R 171

- (2) INFORMATION ON SEQ ID NO. 640:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 161 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

ISRNEGVLVR GPKSPRSLLR SHSEPPALVL WRDHRLVPGT DYCKDTALVP TEKNTGQQEH 60 TFSQYLATPH SELTITHGKW VHSSLWSDPA GLGRQEQHSS SSLSPRQRES LNCKRSGAYT120 VREKEKGGRK GFSPRPPRDA HREGGKEREK SVLESEATLS K

- (2) INFORMATION ON SEQ ID NO. 641:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

CAYRTEKWKS HTVPCSPEVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDCLC 60 RGSTGQPTAN TAASLVSASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120 HHCIPNR

- (2) INFORMATION ON SEQ ID NO. 642:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 136 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

WGXGRVRVXG WXRKPMKXGI PPEXHGPITA DGHRXLXXLP PXGXRCXXAD PKGXGLXALF 60 XKXPPXEXCL LSXXPXXPVT HRAGMEFNGX FWXXTLVHGQ TSLLXGYXTR LKXKIVCCHS120 SGXWSVCGLH RFHRNQ

- (2) INFORMATION ON SEQ ID NO. 643:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

GRXSRAWGLG CPSLLSPISL RLPVPPPRPP NLRPPATPGA PTXPXQNTAX LKXLLELSXX 60 LSGLGLMGXR AGTCTWVAXE AHEDXDTPRV PWTXYXRWSS XPXAIATXGX SLXXGRPQRE120 XPXRVVXKXT TX

- (2) INFORMATION ON SEQ ID NO. 644:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

GVETTANSST SLRSTTLEKE VPVIFIHPLN TGLFRIKIQG ATGKFNMVIP LVDGMIVSRR 60 ALGFLVRQTV INICRRKRLE SDSYSPPMSA GNRKSPTLST STGTSSWSQS FILHFSRRLD120 SRTAVLRPLN F

- (2) INFORMATION ON SEQ ID NO. 645:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLLP RCYFSAGIKL LXVARPRTSK60 DSCYSATVYT AHLSYSHVLS SLVRLF 86

- (2) INFORMATION ON SEQ ID NO. 646:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60 LRSGVLRKFL EPKIRRNPGL SFLRSKMYYQ LRPGEH

- (2) INFORMATION ON SEQ ID NO. 647:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 92 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

SSACRCTTRS TGQQSAASGR CGGPRGWGPS TGATPRQLTM NIPFQSIHFI TYEFLQEQVN60 PHRTYNPQSH IISGGLAGAL AAAARGPLDV LR 92

- (2) INFORMATION ON SEQ ID NO. 648:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 280 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

AVGSAALFKD GGGGTSAAEA GAAGQRLRSV NCLAYDEAIM AQQDRIQQEI AVQNPLVSER 60 LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSHL EALLDDSKEL120 QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180 VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVS1240 QVEYMDRGEG GTTNPHIFPE GSEPKVYLLY RPGHYDILYK

- (2) INFORMATION ON SEQ ID NO. 649:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

DHLQPQKNLC TCLAPGRGGQ QGSSGLEPAL FVEDIVVSRP VEKVDLGLGA LREDVRIGGA 60
ALAAVHVLHL DGHAEGLGQR NDVDVVALLA HGLHLLLAEL LDSPSTLDEV LEELALALQV120
ARGEQPQVDH KVVGGALVIE GGQQVGDRGL LLHLLNQVHE RVVEILNCEF SEALGHQVFL180
ALGRHSLEPL QLLAVIQQCL QVGESESPIE TVAVRPGLAD VRVLFVEVLD LLLIDVVIFS240
ILLV 244

- (2) INFORMATION ON SEQ ID NO. 650:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 424 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

LTTTCVSSSA PSKTSLIMNP HASTNGQLSV HTPKRESLSH EEHPHSHPLY GHGVCKWPGC 60
EAVCEDFQSF LKHLNSEHAL DDRSTAQCRV QMQVVQQLEL QLAKDKERLQ AMMTHLHVKS120
TEPKAAPQPL NLVSSVTLSK SASEASPQSL PHTPTTPTAP LTPVTQGPSV ITTTSMHTVG180
PIRRRYSDKY NVPISSADIA QNQEFYKNAE VRPPFTYASL IRQAILESPE KQLTLNEIYN240
WFTRMFAYFR RNAATWKNAV RHNLSLHKCF VRVENVKGAV WTVDEVEFQK RRPQKISGNP300
SLIKNMQSSH AYCTPLNAAL QASMAENSIP LYTTASMGNP TLGNLASAIR EELNGAMEHT360
NSNESDSSPG RSPMQAVHPV HVKEEPLDPE EAEGPLSLVT TANHSPDFDH DRDYEDEPVN420
EDME

#### (2) INFORMATION ON SEQ ID NO. 651:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

STNAGCTAVR ATACKRQRAP ASHDDPPACE VYRTQSRPSA LESGIKCHSL QVRIGGFSTE 60 LTSYSNDPNR PPDSRHPRPL CHHNHQHAHG GTHPQAVLRQ IQRAHFVSRY CAEPRIL 117

- (2) INFORMATION ON SEQ ID NO. 652:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 426 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

PEAGLFSCSE QSDFPEHIFI MIHTNLKKKF SCCVLVFLLF AVICVWKEKK KGSYYDSFKL 60

QTKEFQVLKS LGKLAMGSDS QSVSSSSTQD PHRGRQTLGS LRGLAKAKPE ASFQVWNKDS120 SSKNLIPRLQ KIWKNYLSMN KYKVSYKGPG PGIKFSAEAL RCHLRDHVNV SMVEVTDFPF180 NTSEWEGYLP KESIRTKAGP WGRCAVVSSA GSLKSSQLGR EIDDHDAVLR FNGAPTANFQ240 QDVGTKTTIR LMNSQLVTTE KRFLKDSLYN EGILIVWDPS VYHSDIPKWY QNPDYNFFNN300 YKTYRKLHPN QPFYILKPQM PWELWDILQE ISPEEIQPNP PSSGMLGIII MMTLCDQVDI360 YESLPSKRKT DVCYYYQKFF DSACTMGAYH PLLYEKNLVK HLNQGTDEDI YLLGKATLPG420 FRTIHC

- (2) INFORMATION ON SEQ ID NO. 653:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

RCVQGSHFVL SRKTSLLIAN PPGAAGPSGP QELALLSMGG KVYWVCRPRP IFLRMIKTHL 60 CWFMVTCAAG FGDAEVCRSI SGGLDAVLPF SLWCWLCGLC GTFCPLARCT LGRGGCGCSA120 RSVAAARSAP TPVGIGSLC 139

- (2) INFORMATION ON SEQ ID NO. 654:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 243 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

WRQLARGWGA LSRASCPALP RLANNTVRMA KGDPKKPKGK MSAYAFFVQT CREEHKKKNP 60
EVPVNFAEFS KKCSERWKTM SGKEKSKFDE MAKADKVRYD REMKDYGPAK GGKKKKDPNA120
PKRPPSGFFL FCSEFRPKIK STNPGISIGD VAKKLGEMWN NLNDSEKQPY ITKTAKLKEK180
YEKDVADYKS KGKFDGAKGP AKVARKKVEE EDEEDGGGGG GGGGGTYSRV GWWSSPKEGE240
RRN

- (2) INFORMATION ON SEQ ID NO. 655:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 110 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

TEQEESRRWP FGSIRILLL ASLSWSIILH FPIIAHFICL CHFIKFRFLF PGHRLPPLRA 60 LLGKFRKIDR DLWVFLLMFF SACLHKEGIS GHLALWFLGV TFSHPDCIVR 110

### (2) INFORMATION ON SEQ ID NO. 656:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 356 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

VGCSHAAQLH SAPELQTTRQ ELSHALYQHD AACRVIARLT KEVTAAREAL ATLKPQAGLI 60
VPQAVPSSQP SVVGAGEPMD LGELVGMTPE IIQKLQDKAT VLTTERKKRG KTVPEELVKP120
EELSKYRQVA SHVGLHSASI PGILALDLCP SDTNKILTGG ADKNVVVFDK SSEQILATLK180
GHTKKVTSVV FHPSQDLVFS ASPDATIRIW SVPNASCVQV VRAHESAVTG LSLHATGDYL240
LSSSDDQYWA FSDIQTGRVL TKVTDETSGC SLTCAQFHPD GLIFGTGTMD SQIKIWDLKE300
RTNVANFPGH SGPITSIAFS ENGYYLATAA DDSSVKLWDL RKLRTLRLCS WITTLR 356

## (2) INFORMATION ON SEQ ID NO. 657:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 240 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

LAQIPELDRG VISRCSQVVT ILREGDASDG ARVAREVGHI STFLQVPDLD LRVHGSCSKD 60 ESVRVELCTG ERAAGGLICH LGEHTPCLDV RESPVLIIGG AQEIVASGMK AEACHSTLMG120 PNHLYTRGIG DRPNPDSGIG GSRKHQVLGR VKHHAGDLLG MAFEGSQDLF RTFVKHNDIF180 IRPTSEDLVG VGRAEVQGQD PRNAGTVQPH VGCHLPVFAE LFWLHQLLRH SLPSLLALRG240

# (2) INFORMATION ON SEQ ID NO. 658:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

EHNSKSSFIN IKRAYLAKDT QIKESLWLRT QGREVPGLCP CWARRLGTK WEKCWEGLSG 60 RGHKSSGGQH CRQVMGGTHG DLAANSCCGG VSLVLPPGGP LLGSWRGPTK GHRTGSPGWL120 VQLGMKAREK RVLCSGRIGP DAEAEALPVT CGRSALSLPG TL 162

- (2) INFORMATION ON SEQ ID NO. 659:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

RLWTAFHGLR AGDEATRRPG LPEHLHGPAV SHRGDGQRDP AYLCWQQERH GAPEERYHPC 60 PGPSQRVPGR DRAERPHVTG SASASASGPI RPLQSTRFSL AFIPSCTNHP GLPVLCPLVG120 PLQEPRSGPP GGSTKDTPPQ QELAARSP